

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:36:28 ; Search time 54 Seconds  
(without alignments)  
596.489 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLLLVLGLWLA.....LSGFLVWRRCRHRSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Description
		Match	Length	
1	607	99.8	114	AAW73409 Human sec
2	571	93.9	129	AAW88506 Human liv
3	571	93.9	129	AAY57940 Human tra
4	571	93.9	129	AAU03498 Human TWE
5	571	93.9	129	ABP61512 Human NF-
6	571	93.9	129	AAU79827 Human typ
7	571	93.9	129	ADA56889 Human sec
8	571	93.9	129	ABU56716 Lung canc
9	571	93.9	129	ADC74112 Human sec
10	571	93.9	129	ADD37867 Human sec
11	571	93.9	129	ADD89033 TAT274. 1
12	450	74.0	129	AAU79828 Mouse typ
13	433	71.2	309	AAU03500 Human TWE
14	274.5	45.1	112	AAY91463 Human sec
15	274.5	45.1	112	ADA57390 Human sec
16	274.5	45.1	112	ADC74462 Human sec
17	274.5	45.1	112	ADD38025 Human sec
18	274.5	45.1	155	AAY91604 Human sec
19	274.5	45.1	155	ADA57391 Human sec
20	274.5	45.1	155	ADC74463 Human sec
21	274.5	45.1	155	ADD38026 Human sec
22	274.5	45.1	156	AAY91552 Human sec
23	191	31.4	32	ADA49370 Human Enl
24	97.5	16.0	171	ADB90668 TALL-1R g
25	97.5	16.0	171	ADB90665 TALL-1R g

26	97.5	16.0	185	7	ADB90663	TALL-1R g
27	97	16.0	170	7	ADB90667	TALL-1R g
28	96.5	15.9	186	7	ADB90675	TALL-1R p
29	94.5	15.5	185	5	AAE22269	Human BAF
30	92.5	15.2	185	5	AAE22267	Human BAF
31	92.5	15.2	185	5	AAE22266	Human BAF
32	91.5	15.0	185	5	AAE22270	Human BAF
33	91.5	15.0	185	5	AAE22271	Human BAF
34	89.5	14.7	185	5	AAE22268	Human BAF
35	88.5	14.6	185	5	AAE22242	Human mat
36	88.5	14.6	1307	7	AAE39974	Human CRU
37	88.5	14.6	1388	5	ABP70118	Human NOV
38	88.5	14.6	1388	5	ABP70117	Human NOV
39	87.5	14.4	185	7	ABR82287	Human BRO
40	87	14.3	184	5	ABB81483	Human Ztn
41	87	14.3	184	6	AAE35227	Human Ztn
42	87	14.3	184	6	ADA49363	Human BAF
43	87	14.3	184	6	ABP97721	Amino aci
44	87	14.3	184	6	ABR61767	Human PRO
45	87	14.3	266	5	AAE22243	Human JST

ALIGNMENTS

RESULT 1  
AAW73409  
ID AAW73409 standard; protein; 114 AA.

XX AAW73409;

XX 19-FEB-1999 (first entry)

DT Human secreted protein encoded by Gene No. 13.

XX Secreted protein; human; protein therapy; gene therapy; blood disorder;  
XX pathologial condition; diagnosis; cancer; neurological disorder;  
XX KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;  
KW immune system disorder; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 114 /note= "unspecified amino acid"

XX W09854206-A1.

XX 03-DEC-1998.

XX 28-MAY-1998; 98WO-US010868.

XX 30-MAY-1997; 97US-0044039P.

XX 30-MAY-1997; 97US-0048093P.

XX 30-MAY-1997; 97US-0048101P.

XX 30-MAY-1997; 97US-0048190P.

XX 30-MAY-1997; 97US-0048356P.

XX 30-MAY-1997; 97US-0050935P.

XX 29-AUG-1997; 97US-0056250P.

XX 29-AUG-1997; 97US-0056293P.

XX 29-AUG-1997; 97US-0056296P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;

XX Ni J, Feng P;

XX WPI; 1999-070209/06.

XX N-PSDB; AAV08823.

XX New isolated human genes - useful for diagnosis and treatment of, e.g.  
PT cancers, neurological disorders, immune diseases, developmental disorders

CC This is the amino acid sequence of a transmembrane protein encoded by  
CC human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a  
CC signal-like N-terminal region and one internal transmembrane domain. The  
CC invention provides nucleotide sequences (see AAV84359-76) coding for 18  
CC transmembrane proteins (see AAW8491-508), vectors containing such  
CC polynucleotides, and eukaryotic cells containing the vectors. The  
CC proteins can be used as antigens or as compositions in the preparation of  
CC antibodies against the proteins. The polynucleotides can be used as  
CC probes for gene diagnosis, and as gene sources for gene therapy and large  
CC -scale production of proteins encoded by the cDNA. The host cells are  
CC used for the detection of ligands corresponding to the expressed  
CC proteins, and the screening of low mol.wt. medicines  
XX  
SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;  
Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db |||||  
QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGSLGFLVWRRRERSPPPP 113  
Db |||||  
61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGSLGFLVWRRRERSPPPP 113

RESULT 3  
AAV57940  
ID AAY57940 standard; protein; 129 AA.

XX AC AAY57940;  
XX DT 23-MAR-2000 (first entry)  
XX DE Human transmembrane protein HTMPN-64.

XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific;  
KW antiproliferative; neuroprotective; immune disorder;  
KW reproductive disorder; smooth muscle disorder; neurological disorder;  
KW gastrointestinal disorder; developmental disorder;  
KW cell proliferative disorder.

XX OS Homo sapiens.

XX PN WO9961471-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011904.

XX PR 29-MAY-1998; 98US-0087260P.

XX PR 02-JUL-1998; 98US-0091674P.

XX PR 02-OCT-1998; 98US-0102954P.

XX PR 24-NOV-1998; 98US-0109869P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;

XX DR WPI; 2000-072605/06.  
XX DR N-PSDB; AAZ56761.

XX Proteins, polynucleotides, vectors, host cells and antibodies used to  
PT diagnose, treat or prevent immune, reproductive, smooth muscle,  
PT neurological, gastrointestinal, developmental and cell proliferative  
PT disorders.

XX Claim 1; Page 163; 229pp; English.

XX AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human

PT or blood disorders.

PS Claim 11; Page 153; 188pp; English.

XX This sequence is encoded by a cDNA of the invention, designated Gene No.  
CC 13. This sequence represents a human secreted protein, and is expressed  
CC in keratinocytes and to a lesser extent in endothelial cells and  
CC placenta. The DNA sequences of the invention and their corresponding  
CC secreted polypeptides are useful for preventing, treating or ameliorating  
CC medical conditions, e.g. by protein or gene therapy. Also pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the DNA sequences. Specific uses are described for each of the DNA  
CC sequences and the encoded proteins, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis or  
CC treatment of cancer, tumours, neurological disorders, developmental  
CC abnormalities and foetal deficiencies, blood disorders, leukaemias,  
CC diseases of the immune system (including allergies or asthma), hepatic  
CC diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate  
CC diseases, autoimmune disorders and AIDS. The polypeptides are also useful  
CC for identifying their binding partners

XX SQ Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db |||||  
QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db |||||

QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGSLGFLVWRRRERSPPPP 113

Db |||||  
61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGSLGFLVWRRRERSPPPP 113

RESULT 2

AAW88506

ID AAW88506 standard; protein; 129 AA.

XX AC AAW88506;

XX DT 30-MAR-1999 (first entry)

XX DE Human liver clone HP10432-encoded membrane protein.

XX KW Transmembrane protein; HP10432; human; liver.

XX OS Homo sapiens.

XX PN WO9855508-A2.

XX PD 10-DEC-1998.

XX PF 03-JUN-1998; 98WO-JP002445.

XX PR 03-JUN-1997; 97JP-00144948.

XX PA (SAGA ) SAGAMI CHEM RES CENTRE.

XX PA (PROT-) PROTEGENE INC.

XX PI Kato S, Sekine S, Yamaguchi T;

XX WPI; 1999-045730/04.

XX N-PSDB; AAV84374.

XX New human proteins containing transmembrane domains and their encoding  
PT sequences - useful in the preparation of antibodies and large-scale  
PT protein production, gene diagnosis, and gene therapy.

XX Claim 1; Page 152-153; 178pp; English.

Example 1; Fig 1; 46pp; English.

Example 1; Fig 1; 46pp; English.

```

Query Match          93.9%; Score 571; DB 4; Length 129;
Best Local Similarity 94.7%; Pred. No. 8.4e-52;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Human: TWEAK receptor (TWEAKR) polypeptide.

1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLKDCKMDCASCRRP 60

1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLKDCKMDCASCRRP 60

ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis.

[illegible]

## RESULT 5

ABP61512

1312  
ABP61512 standard: protein; 129 AA.

ABP61512;

ABP61512;

30-SEP-2002 (first entry)

Human NF- $\kappa$ B activating protein SEQ ID NO 178.

Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic; neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; Arns. neurodegenerative disease; ischaemic disorder.

**Homo sapiens.**

**Homo sapiens.**

WO200253737-A1.

WO200253737-A1.

17-III.-2002.

17-III.-2002.

11-JUL-2002.

11-JUL-2002.

11-JUL-2002.

11-JUL-2002.

25-DEC-2001: 2001WO-JP011389.

25-DEC-2001: 2001WO-JP011389.

25-DEC-2001: 2001WO-JP011389.

28-DEC-2000; 2000JP-00402288.

28-DEC-2000; 2000JP-00402288.

28-DEC-2000; 2000JP-00402288.

(ASAHI) ASAHI KASEI KOGYO KK.

Matsumida A, Honda G, Muramatsu S, Nagano Y;

Matsumida A, Honda G, Muramatsu S, Nagano Y;

Matsumida A, Honda G, Muramatsu S, Nagano Y;

DR WPI; 2002-583617/62.  
DR N-PSDB; ABQ92000.  
XX  
PT NF-approximatelykB activating gene and expressed protein, applicable in  
PT diagnosis and screening inhibitors or promoters to control excessive  
PT activation or inhibition for treating e.g. inflammations, autoimmune  
PT diseases and cancer.  
XX  
PS Claim 4; Page 814-815; 841pp; Japanese.  
XX  
CC The invention relates to a purified protein (I), comprising one of 90  
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
CC the sequences but with some amino acids deleted, substituted or added and  
CC with a NF-KB (nuclear factor kappa B) activating effect. The protein and  
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
CC inhibitors or promoters to control excessive activation or inhibition and  
CC for treating e.g. inflammations, autoimmune diseases, cancers, or ischaemic  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 5; Length 129;  
Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113  
RESULT 6  
AAU79827  
ID AAU79827 standard; protein; 129 AA.  
XX  
AC AAU79827;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human type 1 transmembrane protein Fn14.  
XX  
KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
XX  
OS Homo sapiens.  
XX  
PN WO200222166-A2.  
XX  
PF 21-MAR-2002.  
XX  
PD 12-SEP-2001; 2001WO-US028451.  
XX  
PR 14-SEP-2000; 2000US-0232355P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Browning J, Burkly L, Jakubowski A, Zheng T;  
XX  
DR WPI; 2002-383103/41.  
XX  
PT Methods of modulating angiogenesis and inhibiting tumor progression,  
PT using TWEAK receptor agonists.  
XX  
PS Disclosure; Fig 10A; 37pp; English.

XX The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 5; Length 129;  
Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113  
RESULT 7  
ADA56889  
ID ADA56889 standard; protein; 129 AA.  
XX  
AC ADA56889;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein #172.  
XX  
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
OS Homo sapiens.  
XX  
PN WO2002102994-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008278.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-167512/16.  
DR N-PSDB; ADA55993.  
XX  
PT New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX



XX  
KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;  
KW antiparkinsonian; neuroprotective; nontropic; antibacterial; virucide;  
KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;  
KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

KW human.  
XX  
OS Homo sapiens.  
XX  
FN WO2003038063-A2.  
XX  
PD 08-MAY-2003.  
XX  
PF 19-MAR-2002; 2002WO-US008277.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
PI WPI; 2003-430516/40.  
DR N-PSDB; ADC73497.  
XX  
PT New human secreted polypeptide for diagnosing, preventing or treating  
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
PT atherosclerosis).  
XX  
PS Claim 16; SEQ ID NO 745; 2272pp; English.  
XX  
CC The invention relates to a novel human secreted polypeptide comprising a  
CC defined sequence given in the specification. The polypeptide, nucleic  
CC acid molecule, antibody, agonist or antagonist of the invention may be  
CC useful for preparing a composition for diagnosing or treating a  
CC haemopoietic or haematologic disorder such as anaemia, autoimmune  
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
CC disease, wounds and hyperproliferative disorders including  
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
CC parasitic infections. The polypeptide may also be used during gene  
CC therapy procedures and for identifying a binding partner by contacting  
CC the polypeptide with a binding partner and determining whether the  
CC binding partner increases or decreases the activity of the polypeptide.  
CC The current sequence is that of the human secreted protein of the  
CC invention.  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 7; Length 129;  
Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113  
RESULT 10  
ADD37867  
ID ADD37867 standard; protein; 129 AA.  
XX  
AC ADD37867;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human secreted protein #50.  
XX  
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;  
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.  
XX

OS Homo sapiens.  
XX  
PN WO200290526-A2.  
XX  
PD 14-NOV-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008279.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
PI WPI; 2003-140218/13.  
XX  
PT New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing or  
PT treating allergic or asthmatic disorders, or related immediate  
PT hypersensitivity disorders.  
XX  
PS Claim 1; SEQ ID NO 349; 1323pp; English.  
XX  
CC The present invention relates to an isolated polypeptide or human  
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or  
CC their fragments, and agonists or antagonists that bind are useful for  
CC preparing a diagnostic or pharmaceutical composition for diagnosing or  
CC treating allergic or asthmatic disorders. The polypeptide is also useful  
CC for identifying a binding partner by contacting the polypeptide with a  
CC binding partner, and determining whether the binding partner increases or  
CC decreases the activity of the polypeptide. The polypeptides and nucleic  
CC acid molecules are also useful for detecting, preventing, diagnosing,  
CC prognosticating, treating or ameliorating inflammatory disorders  
CC neoplastic diseases, wound healing and disorders of epithelial cell  
CC proliferation, immune disorders, cardiovascular disorders, blood-related  
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal  
CC disorders. The nucleic acids are also useful for chromosome  
CC identification, radiation hybrid mapping or long-range restriction  
CC mapping, as molecular weight markers, or as hybridization or diagnostic  
CC probes. The polypeptides and antibodies are useful for providing  
CC immunological probes for differential identification of the tissues  
CC immunohistochemistry assays. The present sequence represents a human  
CC secreted protein.  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 7; Length 129;  
Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113  
RESULT 11  
ADD89033  
ID ADD89033 standard; protein; 129 AA.  
XX  
AC ADD89033;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE TAT274.  
XX  
KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;  
KW cancer.









Query Match 45.1%; Score 274.5; DB 3; Length 112;  
Best Local Similarity 96.4%; Pred. No. 7.2e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
DB 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56  
  
RESULT 15  
ADA57390  
ID ADA57390 standard; protein; 112 AA.  
AC ADA57390;  
XX  
DT 20-NOV-2003 (first entry)  
XX Human secreted protein #172.  
DE  
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
QS Homo sapiens.  
XX  
PN WO2002102994-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008278.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2003-167512/16.  
DR N-PSDB; ADA56496.  
DR  
XX  
PT New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX  
PS Claim 13; SEQ ID NO 1582; 1754pp; English.  
XX  
CC The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals

CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence corresponds  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 112 AA;  
  
Query Match 45.1%; Score 274.5; DB 6; Length 112;  
Best Local Similarity 96.4%; Pred. No. 7.2e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
DB 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56  
  
Search completed: March 1, 2004, 16:42:52  
Job time : 77 secs

GenCore version 5.1.6  
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OMprotein - protein search, using sw model

Run on: March 1, 2004, 16:41:53 ; Search time 23 Seconds  
(without alignments)  
255.885 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLRLVLGLWLA.....LSGFLVWRRRCRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	274.5	45.1	155	4	US-09-489-847-284
4	274.5	45.1	156	4	US-09-489-847-288
5	96.5	15.9	248	4	US-09-252-991A-29249
6	88.5	14.6	400	4	US-09-252-991A-26145
7	87.5	14.4	631	4	US-09-252-991A-20063
8	83.5	13.7	152	4	US-09-252-991A-31619
9	80.5	13.2	249	4	US-09-252-991A-29850
10	76.5	12.6	250	4	US-09-322-409-31
11	76.5	12.6	250	4	US-09-451-527-31
12	76.5	12.6	276	4	US-09-322-409-26
13	76.5	12.6	276	4	US-09-451-527-26
14	75	12.3	334	4	US-09-252-991A-18795
15	74.5	12.3	305	4	US-09-252-991A-21147
16	73.5	12.1	187	4	US-09-199-637A-287
17	73.5	12.1	187	4	US-09-252-991A-21454
18	72	11.8	1278	4	US-09-462-136-2
19	72	11.8	3724	2	US-08-804-227C-10
20	72	11.8	3724	2	US-08-804-198-4
21	71.5	11.8	478	4	US-09-252-991A-22078
22	70.5	11.6	402	4	US-09-252-991A-18195
23	69.5	11.4	176	4	US-09-252-991A-25290
24	69	11.3	152	4	US-09-252-991A-24730
25	69	11.3	153	4	US-09-252-991A-20688
26	69	11.3	215	3	US-09-220-528-104
27	69	11.3	511	4	US-09-252-991A-28223

28	68.5	11.3	127	4	US-09-489-039A-10884	Sequence 10884, A
29	68.5	11.3	205	2	US-08-775-009-37	Sequence 37, Appl
30	68.5	11.3	429	1	US-07-964-589-2	Sequence 2, Appli
31	68.5	11.3	429	5	PCT-US93-02024-2	Sequence 2, Appli
32	68	11.2	139	4	US-09-252-991A-17414	Sequence 17414, A
33	68	11.2	144	4	US-09-252-991A-17313	Sequence 17313, A
34	68	11.2	204	4	US-09-252-991A-29996	Sequence 29996, A
35	68	11.2	282	4	US-09-252-991A-29124	Sequence 29124, A
36	68	11.2	366	4	US-09-252-991A-31958	Sequence 31958, A
37	68	11.2	775	4	US-09-252-991A-22300	Sequence 22300, A
38	67.5	11.1	174	3	US-09-383-586-12	Sequence 12, Appl
39	67.5	11.1	268	4	US-09-322-409-23	Sequence 23, Appl
40	67.5	11.1	268	4	US-09-451-527-23	Sequence 23, Appl
41	67.5	11.1	294	4	US-09-322-409-7	Sequence 7, Appli
42	67.5	11.1	294	4	US-09-451-527-7	Sequence 7, Appli
43	67.5	11.1	359	3	US-09-413-814-90	Sequence 90, Appl
44	67.5	11.1	361	3	US-09-413-814-77	Sequence 77, Appl
45	67	11.0	112	4	US-09-252-991A-21707	Sequence 21707, A

ALIGNMENTS

RESULT 1  
US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: xaa equals stop translation  
US-09-690-454-59

Query Match 99.8%; Score 607; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.5e-59;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Db 1 MARGSLRRLRLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLLWPILGGALSLTFVLGLLSGFLVWRRCRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLLWPILGGALSLTFVLGLLSGFLVWRRCRRSSPPP 113

RESULT 2  
US-09-489-847-139  
; Sequence 139, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-139

Query Match 45.1%; Score 274.5; DB 4; Length 112;  
Best Local Similarity 96.4%; Pred. No. 8.9e-23;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 3  
US-09-489-847-284  
; Sequence 284, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 284  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-284

Query Match 45.1%; Score 274.5; DB 4; Length 155;  
Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 4  
US-09-489-847-228  
; Sequence 228, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 228  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (156)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-489-847-228

Query Match 45.1%; Score 274.5; DB 4; Length 156;  
Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 5  
US-09-252-991A-29249  
; Sequence 29249, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29249  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29249

Query Match 15.9%; Score 96.5; DB 4; Length 248;  
Best Local Similarity 30.0%; Pred. No. 0.007;  
Matches 27; Conservative 9; Mismatches 23; Indels 31; Gaps 4;  
QY 18 WLALLRSVAGE-----QAPGTAPCSRG-----SWSADLDKCM 50  
Db 38 WCSSTRSGGAACRRCCRASSTAPCSRASPSATAAPRTRTGSNCWAGAAPTCWSATTSRCR 97  
QY 51 DCASCRARPHSD-FCLGCA---AAPPAPER 76  
Db 98 GCASSRRARRRTGRWCAACSAAPVASPPAAWK 127

RESULT 6

US-09-252-991A-26145  
; Sequence 26145, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26145  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26145

Query Match 14.6%; Score 88.5; DB 4; Length 400;  
Best Local Similarity 38.3%; Pred. No. 0.091;  
Matches 23; Conservative 4; Mismatches 30; Indels 3; Gaps 2;  
QY 18 WLALLRSVAGEQAPGTAPCS--RGSSWSADLDKCMDCASCRRARPHSDFCLGCA-AAPPAP 74  
Db 45 WSTAWREFPAPATAAGWPRCAWPMASNWTATLSPTSTASCRPMPHRCSCACCAKSRPPAP 104

RESULT 7

US-09-252-991A-20063  
; Sequence 20063, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20063  
; LENGTH: 631  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20063

Query Match 14.4%; Score 87.5; DB 4; Length 631;  
Best Local Similarity 32.6%; Pred. No. 0.2;  
Matches 30; Conservative 6; Mismatches 43; Indels 13; Gaps 4;  
QY 23 RSVAGEQAPGTAPCSRG-SWS-ADLDKCM--DCASCRARPHSDFCLGCAAPPAPFRL 78

Db 112 RSSRKSrvPPAWPCVRGSRDWOQAPMRACCRGSCATCSATP-----AATPSAAACC 162  
QY 79 WPILGGALSLTFVLGLLSGFLVWRRCCRERSS 110  
Db 163 WGRAGVAARYAWRCGTLAGASPTSCRRSSSS 194

RESULT 8

US-09-252-991A-31619  
; Sequence 31619, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31619  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31619

Query Match 13.7%; Score 83.5; DB 4; Length 152;  
Best Local Similarity 29.7%; Pred. No. 0.11;  
Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;

QY 23 RSVAGEQAPGTAPCSRGSSWSADLDKMDC-----ASC--RAPPHSDFCLGCAAPPAP 74  
Db 63 RTTSNASRPTPARCSRHAPGWLSTRCACCGAAACGASCATARTPT-----TAAWPPSS 117  
QY 75 FRLLWPILGGALSLTFVLGLLSGFLVWRRCRRE---RSSPP 112  
Db 118 APATWSASGGRCAGN-----WRRCNRAWGWRQSP 147

RESULT 9

US-09-252-991A-29850  
; Sequence 29850, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29850  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29850

Query Match 13.2%; Score 80.5; DB 4; Length 249;  
Best Local Similarity 30.5%; Pred. No. 0.4;  
Matches 40; Conservative 8; Mismatches 32; Indels 51; Gaps 8;

QY 10 LRLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC-----RA 57  
Db 104 LRAVRLAAPFCLLRAVAGARLVAAAP--RGAGLAAPAQS--PAASCSANTSRSTFAPLRI 159





; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-451-527-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;  
Best Local Similarity 27.5%; Pred. No. 1.2;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;  
QY 11 RLLVLGLWLLALRSVAG-----EQAPGTAPCSRGSSWSA 44  
Db 75 RLVLQRMVRLQAVAGSQMQLLEAVNTEIHFTVFCAFQDTSQQLAALKPWITRRNFSG 134  
QY 45 DLD-KCMDASCARPHSDFCLGCAA--APPAPFRLLPILGGALSULTFVLGLLSGFLVW 101  
Db 135 CLELQCPDSSSTLVPPRSPGALEATALPAPQAP-RLLLLLL---LPVALLMSTAWCLHW 190  
QY 102 RRCRRRSSPP 112  
Db 191 RRRRRRRSPYP 201

RESULT 14

US-09-252-991A-18795  
; Sequence 18795, Application US/09252991A  
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18795  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18795

Query Match 12.3%; Score 75; DB 4; Length 334;  
Best Local Similarity 35.6%; Pred. No. 2.2;  
Matches 26; Conservative 7; Mismatches 30; Indels 10; Gaps 4;  
QY 33 TAPCSRGSSWSADLDKCMDCASCARPHSDFCLGCAAAPAPFR--LLWPILGGALSITF 90  
Db 38 TTPTTSTARWSRPVP-----APCLQAPAS--LLSTSTAPTATMADELLNALLAG-LALAL 89  
QY 91 VLGLLSGFLVWRR 103  
Db 90 VAGPLGSFVWRR 102

RESULT 15

US-09-252-991A-21147  
; Sequence 21147, Application US/09252991A  
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21147  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21147

Query Match 12.3%; Score 74.5; DB 4; Length 305;  
Best Local Similarity 29.1%; Pred. No. 2.3;  
Matches 37; Conservative 10; Mismatches 61; Indels 19; Gaps 4;  
QY 3 RGSRLRLRLLLVLGLWL-----ALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRR 58  
Db 20 RPSITTRKPPAMCSLTLLWLAESTAAPVPSWACSESPETLVMLRSMWATWLCSSAAVAICWLR 79  
QY 59 PHSDFCIGCA-----AAPPAPFRLIW-----PILGGALSIT-----FVLGLLSGFLVWRR 103  
Db 80 PSSSSTVATMRPSSAWAALSASTRLLWAWLALPRMAATASLAPSCNCSINPWISWVDCWVR 139  
QY 104 CRRERSS 110  
Db 140 LASERTS 146

Search completed: March 1, 2004, 16:45:09  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:43:58 ; Search time 33 Seconds  
(without alignments)  
729.439 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLLLVGLWLA.....LSGFLVWRRRCRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

\*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	99.8	114	14	US-10-062-831-59
2	607	99.8	114	14	US-10-062-599-59
3	571	93.9	129	9	US-09-742-454A-4
4	571	93.9	129	9	US-09-883-777-4
5	571	93.9	129	14	US-10-024-298A-178
6	571	93.9	129	14	US-10-042-211A-178
7	571	93.9	129	15	US-10-331-496A-37
8	571	93.9	129	15	US-10-295-027-444
9	571	93.9	129	15	US-10-295-027-1305
10	450	74.0	129	9	US-09-742-454A-5
11	450	74.0	129	9	US-09-883-777-5
12	433	71.2	309	9	US-09-742-454A-7
13	433	71.2	309	9	US-09-883-777-7
14	379.5	62.4	300	9	US-09-883-777-9
15	97.5	16.0	171	14	US-10-251-947-4

16	97.5	16.0	171	14	US-10-251-947-7	Sequence 7, Appli
17	97.5	16.0	185	14	US-10-251-947-2	Sequence 2, Appli
18	97	16.0	170	14	US-10-251-947-6	Sequence 6, Appli
19	96.5	15.9	186	14	US-10-251-947-14	Sequence 14, Appli
20	88.5	14.6	1307	14	US-10-303-685-17	Sequence 17, Appli
21	88.5	14.6	1388	15	US-10-093-463-138	Sequence 138, App
22	88.5	14.6	1388	15	US-10-093-463-140	Sequence 140, App
23	87	14.3	184	14	US-10-008-063-2	Sequence 2, Appli
24	87	14.3	184	14	US-10-152-363A-60	Sequence 60, Appli
25	79.5	13.1	377	14	US-10-156-761-8962	Sequence 8962, Ap
26	76.5	12.6	250	14	US-10-218-654-31	Sequence 31, Appli
27	76.5	12.6	250	14	US-10-262-439-31	Sequence 31, Appli
28	76.5	12.6	276	14	US-10-218-654-26	Sequence 26, Appli
29	76.5	12.6	276	14	US-10-262-439-26	Sequence 26, Appli
30	76.5	12.6	732	14	US-10-156-761-12251	Sequence 12251, A
31	75.5	12.4	287	15	US-10-108-260A-3127	Sequence 3127, Ap
32	75.5	12.4	287	15	US-10-108-260A-3845	Sequence 3845, Ap
33	75.5	12.4	635	15	US-10-369-493-5911	Sequence 5911, Ap
34	75.5	12.4	635	15	US-10-369-493-5912	Sequence 5912, Ap
35	75	12.3	356	15	US-10-085-198-64	Sequence 64, Appli
36	74	12.2	548	15	US-10-434-156-12	Sequence 12, Appli
37	74	12.2	768	15	US-10-369-493-5165	Sequence 5165, Ap
38	73.5	12.1	187	10	US-09-975-719-287	Sequence 287, App
39	73.5	12.1	409	14	US-10-156-761-11890	Sequence 11890, A
40	72.5	11.9	242	9	US-09-738-626-6004	Sequence 6004, Ap
41	72.5	11.9	365	10	US-09-860-836B-5	Sequence 5, Appli
42	72.5	11.9	365	14	US-10-436-523-59	Sequence 59, Appli
43	72.5	11.9	391	15	US-10-264-049-2579	Sequence 2579, Ap
44	72	11.8	257	15	US-10-104-047-3192	Sequence 3192, Ap
45	72	11.8	1278	14	US-10-208-731-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-10-062-831-59  
; Sequence 59, Application US/10062831  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062,831  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: SITE  
LOCATION: (114)  
OTHER INFORMATION: Xaa equals stop translation  
US-10-062-831-59

Query Match 99.8%; Score 607; DB 14; Length 114;

Best Local Similarity 100.0%; Pred. No. 1.8e-51;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

DB 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 2

US-10-062-599-59

Sequence 59, Application US/10062599  
Publication No. US20030195346A1

GENERAL INFORMATION:

APPLICANT: Steven M. Ruben, et al.  
TITLE OF INVENTION: 32 Human Secreted Proteins  
FILE REFERENCE: PZ006PI

CURRENT APPLICATION NUMBER: US/10/062,599

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: 09/690,454

PRIOR FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: 09/189,144

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: 60/044,039

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,093

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,190

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/050,935

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,101

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,356

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/056,250

PRIOR FILING DATE: August 29, 1997

PRIOR APPLICATION NUMBER: 60/056,296

PRIOR FILING DATE: August 29, 1997

PRIOR APPLICATION NUMBER: 60/056,293

PRIOR FILING DATE: August 29, 1997

NUMBER OF SEQ ID NOS: 229

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 59

LENGTH: 114

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (114)

OTHER INFORMATION: Xaa equals stop translation

US-10-062-599-59

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e-51;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 3

US-09-742-454A-4

Sequence 4, Application US/09742454A  
Patent No. US20020041876A1

GENERAL INFORMATION:

APPLICANT: WILEY, Steven R.

TITLE OF INVENTION: TWEAK Receptor

FILE REFERENCE: 2968-B

CURRENT APPLICATION NUMBER: US/09/742,454A

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/172,878

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: 60/203,347

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 129

TYPE: PRT

ORGANISM: Homo sapiens

US-09-742-454A-4

Query Match

Best Local Similarity 93.9%; Score 571; DB 9; Length 129;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

DB 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 4

US-09-883-777-4

Sequence 4, Application US/09883777  
Patent No. US20020110853A1

GENERAL INFORMATION:

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: TWEAK RECEPTOR

FILE REFERENCE: 2968-C

CURRENT APPLICATION NUMBER: US/09/883,777

CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 60/172,878

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: PCT/US00/34755

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 09/742,454

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 129

TYPE: PRT

ORGANISM: homo sapiens

US-09-883-777-4

Query Match

Best Local Similarity 93.9%; Score 571; DB 9; Length 129;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113



Db 61 SDFCLGCAAAPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRRREKFTTP 113

RESULT 5

US-10-024-298A-178  
; Sequence 178, Application US/10024298A  
; Publication No. US20030143540A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA  
; APPLICANT: AKIO MATSUDA  
; APPLICANT: GOICHI HONDA  
; APPLICANT: SHUJI MURAMATSU  
; APPLICANT: YUKIKO NAGANO  
; TITLE OF INVENTION: NF-K B Activating Gene  
; FILE REFERENCE: 1254-0191P  
; CURRENT APPLICATION NUMBER: US/10/024,298A  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/278,641  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP0088912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-298A-178

Query Match 93.9%; Score 571; DB 14; Length 129;  
Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRRREKFTTP 113  
Db 61 SDFCLGCAAAPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRRREKFTTP 113

RESULT 6

US-10-042-211A-178  
; Sequence 178, Application US/10042211A  
; Publication No. US20030170719A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFkB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24

; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-211A-178

Query Match 93.9%; Score 571; DB 14; Length 129;  
Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
QY 61 SDFCLGCAAAPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRRREKFTTP 113  
Db 61 SDFCLGCAAAPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRRREKFTTP 113

RESULT 7

US-10-331-496A-37  
; Sequence 37, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WU, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TREATMENT OF TUMOR  
; FILE REFERENCE: P5014R1-PCT  
; CURRENT APPLICATION NUMBER: US/10/331,496A  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/345,444  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US 60/351,885  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/360,066  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US 60/362,004  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/366,869  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,284  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/368,679  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 37  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-331-496A-37

Query Match 93.9%; Score 571; DB 15; Length 129;  
Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Qy	61	SDFCLGCAAPAPFRLWPILGGALSTFVLGLLSGFLVWRR	RRRRSSPPP	113
Db	61	SDFCLGCAAPAPFRLWPILGGALSTFVLGLLSGFLVWRR	RRRRKFTTP	113

## RESULT 8

US-10-295-027-444  
; Sequence 444, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynnne, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.

Query Match	93.9%	Score 571;	DB 15;	Length 129;
Best Local Similarity	94.7%	Pred. No. 6.3e-48;		
Matches 107; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY 1 MARGSLRRLLRVLGWLALLRRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRAPH 60

Qb 1 MARGSLRRLLRVLGWLALLRRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRAPH 60

Qy	61	SDFCLGCAAPPAPRLLWPILGGALS	TFVLGLLSGFLVWRR	CRRRERSPPP	113
db	61	SDFCLGCAAPPAPRLLWPILGGALS	TFVLGLLSGFLVWRR	CRRREREKTFP	113

## RESULT. T 9

US-10-2995-027-1305  
; Sequence 1305, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel

```

; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-1305

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Query Match 93.9%; Score 571; DB 15; Length 129;  
Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY											
n6	1	MARGSLRLRL <th>LLVGL</th> <th>WLALL</th> <th>RSVAGE</th> <th>QPGTAP</th> <th>PCSRGSS</th> <th>WSADLD</th> <th>KCMDCAS</th> <th>CRAPH</th> <th>60</th>	LLVGL	WLALL	RSVAGE	QPGTAP	PCSRGSS	WSADLD	KCMDCAS	CRAPH	60

QY	61	SDFCLGCAAPAPFRLLWPI	LGALSLTFVLG	LLSGFLVWRR	CRRRERSDPP	113
QY	61	SDFCLGCAAPAPFRLLWPI	LGALSLTFVLG	LLSGFLVWRR	CRRRERSDPP	113
ph	61	SDFCLGCAAPAPFRLLWPI	LGALSLTFVLG	LLSGFLVWRR	CRRREREKFTTP	113

RESIST 10

US-09-742-454A-5  
; Sequence 5, Application US/09742454A  
; Patent No. US20020041876A1  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5

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; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match          74.0%; Score 450; DB 9; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.4e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

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    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113
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Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLVLVLALVSSFLVWRRRERREKFTTP 113
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RESULT 11
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match          74.0%; Score 450; DB 9; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.4e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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Db 1 MAPGWPRSLPQILVLGFLVLMRAAAGEQAPGTSPCSSGSSWSADLDKCMDCASCRRPH 60
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QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113
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Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLVLVLALVSSFLVWRRRERREKFTTP 113
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RESULT 12
US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match          71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.7e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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Db 1 MARGSLRRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 112
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Db 61 SDFCLGCAAAAPPAPFRLL-----WRSCDKTHTCPP 90
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RESULT 13
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match          71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.7e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 112
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Db 61 SDFCLGCAAAAPPAPFRLL-----WRSCDKTHTCPP 90
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RESULT 14
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
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; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-9

Query Match 62.4%; Score 379.5; DB 9; Length 300;  
Best Local Similarity 88.0%; Pred. No. 5.6e-29;  
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;  
  
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RESULT 15  
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; Sequence 4, Application US/10251947  
; Publication No: US20030099990A1  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof  
; FILE REFERENCE: 01-1160-A  
; CURRENT APPLICATION NUMBER: US/10/251,947  
; CURRENT FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-251-947-4

Query Match 16.0%; Score 97.5; DB 14; Length 171;  
Best Local Similarity 31.8%; Pred. No. 0.071;  
Matches 34; Conservative 9; Mismatches 39; Indels 25; Gaps 5;  
  
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Job time : 47 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:42:58 ; Search time 181 Seconds  
(without alignments)  
614.752 Million cell updates/sec

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Perfect score: 608  
Sequence: 1 MARGSLRRLRLRLVLGLWLA.....LSGFLVWRCRRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 6019581

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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33: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	607	99.8	114	1	PCT-US98-10868-60	Sequence 60, Appl
2	607	99.8	114	15	US-09-189-144-59	Sequence 59, Appl
3	607	99.8	114	26	US-10-062-599-59	Sequence 59, Appl
4	607	99.8	114	26	US-10-062-831-59	Sequence 59, Appl
5	571	93.9	129	1	PCT-US02-08277-745	Sequence 745, App
6	571	93.9	129	1	PCT-US02-08278-1079	Sequence 1079, Ap
7	571	93.9	129	1	PCT-US02-08279-349	Sequence 349, App
8	571	93.9	129	1	PCT-US02-41798A-37	Sequence 37, Appl
9	571	93.9	129	17	US-09-307-140-627	Sequence 627, App
10	571	93.9	129	17	US-09-316-633-265	Sequence 265, App
11	571	93.9	129	18	US-09-445-258-16	Sequence 16, Appl
12	571	93.9	129	18	US-09-445-258A-16	Sequence 16, Appl
13	571	93.9	129	18	US-09-465-587-220	Sequence 220, App
14	571	93.9	129	21	US-09-700-590A-64	Sequence 64, Appl
15	571	93.9	129	21	US-09-742-454A-4	Sequence 4, Appli
16	571	93.9	129	23	US-09-817-076-627	Sequence 627, App
17	571	93.9	129	23	US-09-883-777-4	Sequence 4, Appli
18	571	93.9	129	24	US-09-949-016-6914	Sequence 6914, Ap
19	571	93.9	129	26	US-10-024-298A-178	Sequence 178, App
20	571	93.9	129	26	US-10-042-211A-178	Sequence 178, App
21	571	93.9	129	27	US-10-126-052A-631	Sequence 631, App
22	571	93.9	129	28	US-10-295-027-444	Sequence 444, App
23	571	93.9	129	28	US-10-295-027-1305	Sequence 1305, Ap
24	571	93.9	129	29	US-10-331-496A-37	Sequence 37, Appl
25	571	93.9	129	30	US-10-405-027-4882	Sequence 4882, Ap
26	571	93.9	129	31	US-10-617-217A-178	Sequence 178, App
27	571	93.9	129	31	US-10-626-686-16	Sequence 16, Appl
28	571	93.9	129	33	US-60-109-869-2	Sequence 2, Appli
29	450	74.0	129	21	US-09-742-454A-5	Sequence 5, Appli
30	450	74.0	129	23	US-09-883-777-5	Sequence 5, Appli
31	433	71.2	309	21	US-09-742-454A-7	Sequence 7, Appli
32	433	71.2	309	23	US-09-883-777-7	Sequence 7, Appli
33	379.5	62.4	300	23	US-09-883-777-9	Sequence 9, Appli
34	336.5	55.3	94	30	US-10-405-027-4883	Sequence 4883, Ap
35	336.5	55.3	94	30	US-10-405-027-4884	Sequence 4884, Ap
36	274.5	45.1	112	1	PCT-US02-08277-1095	Sequence 1095, Ap
37	274.5	45.1	112	1	PCT-US02-08278-1582	Sequence 1582, Ap
38	274.5	45.1	112	1	PCT-US02-08279-507	Sequence 507, App
39	274.5	45.1	112	1	PCT-US99-17130-136	Sequence 136, App
40	274.5	45.1	112	29	US-10-351-334-139	Sequence 139, App
41	274.5	45.1	112	30	US-10-405-027-3456	Sequence 3456, Ap
42	274.5	45.1	155	1	PCT-US02-08277-1096	Sequence 1096, Ap
43	274.5	45.1	155	1	PCT-US02-08278-1583	Sequence 1583, Ap
44	274.5	45.1	155	1	PCT-US02-08279-508	Sequence 508, App
45	274.5	45.1	155	1	PCT-US99-17130-277	Sequence 277, App

ALIGNMENTS

RESULT 1  
PCT-US98-10868-60  
; Sequence 60, Application PC/TUS9810868  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc., et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/10868  
; FILING DATE: May 27, 1998  
; CLASSIFICATION:



RESULT 5  
PCT-US02-08277-745  
; Sequence 745, Application PC/TUS0208277  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS907PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/08277  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: US 60/331,287  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/306,171  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/277,340  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 1357  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 745  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-08277-745

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RESULT 7
PCT-US02-08279-349
; Sequence 349, Application PC/TUS0208279
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS903PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08279
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 642
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 349
; LENGTH: 129
; TYPE: PR1
; ORGANISM: Homo sapiens
PCT-US02-08279-349

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Query Match 93.9%; Score 571; DB 1; Length 129;

Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 8  
PCT-US02-41798A-37  
; Sequence 37, Application PC/TUS0241798A  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WU, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5014R1-PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/41798A  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/345,444  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US 60/351,885  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/360,066  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US 60/362,004  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/366,869  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,284  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/368,679  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 37  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapien

PCT-US02-41798A-37  
Query Match 93.9%; Score 571; DB 1; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 9  
US-09-307-140-627  
; Sequence 627, Application US/09307140  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.

APPLICANT: Holtzman, Douglas A.  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a  
TITLE OF INVENTION: Human Aortic Endothelium Library  
FILE REFERENCE: MLN98-14pA  
CURRENT APPLICATION NUMBER: US/09/307,140  
CURRENT FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: 60/084,565  
EARLIER FILING DATE: 1998-05-07  
NUMBER OF SEQ ID NOS: 1168  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 627  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(27)  
US-09-307-140-627

Query Match 93.9%; Score 571; DB 17; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 10  
US-09-316-633-265  
; Sequence 265, Application US/09316633  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Derived from a  
; TITLE OF INVENTION: Human Mesangial Cell Library  
; FILE REFERENCE: MLN98-16pA  
; CURRENT APPLICATION NUMBER: US/09/316,633  
; CURRENT FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/087,052  
; PRIOR FILING DATE: 1998-05-27  
; NUMBER OF SEQ ID NOS: 422  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 265  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(27)  
US-09-316-633-265

Query Match 93.9%; Score 571; DB 17; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWLPILGGALSLTFVLGLLSGFLVWRRRERSPPPP 113

RESULT 11  
US-09-445-258-16



; Sequence 16, Application US/09445258

; GENERAL INFORMATION:

; APPLICANT: Kato, Seishi

; APPLICANT: Sekine, Shingo

; APPLICANT: Kimura, Tomoko

; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE

; TITLE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PROTEINS

; FILE REFERENCE: GIN-6706CPUS

; CURRENT APPLICATION NUMBER: US/09/445,258

; CURRENT FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: PCT/US98/02445

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: JP 9-144948

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-445-258-16

Query Match 93.9%; Score 571; DB 18; Length 129;

Best Local Similarity 94.7%; Pred. No. 3.3e-47;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

Db 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

QY 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113

|||||

Db 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113

|||||

#### RESULT 12

US-09-445-258A-16

; Sequence 16, Application US/09445258A

; GENERAL INFORMATION:

; APPLICANT: Kato, Seishi

; APPLICANT: Sekine, Shingo

; APPLICANT: Kimura, Tomoko

; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE

; TITLE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PROTEINS

; FILE REFERENCE: GIN-6706CPUS

; CURRENT APPLICATION NUMBER: US/09/445,258A

; CURRENT FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: PCT/US98/02445

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: JP 9-144948

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-445-258A-16

Query Match 93.9%; Score 571; DB 18; Length 129;

Best Local Similarity 94.7%; Pred. No. 3.3e-47;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

Db 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

QY 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113

|||||

Db 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113

|||||

#### RESULT 13

US-09-465-587-220

; Sequence 220, Application US/09465587

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

; TITLE OF INVENTION: HUMAN ADULT EPIDERMAL KERATINOCYTE LIBRARY

; FILE REFERENCE: 1600.1080-001

; CURRENT APPLICATION NUMBER: US/09/465,587

; CURRENT FILING DATE: 1999-12-17

; PRIOR APPLICATION NUMBER: 60/114,591

; PRIOR FILING DATE: 1998-12-31

; NUMBER OF SEQ ID NOS: 356

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 220

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(27)

; US-09-465-587-220

Query Match 93.9%; Score 571; DB 18; Length 129;

Best Local Similarity 94.7%; Pred. No. 3.3e-47;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

Db 1 MARGSLRLLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

|||||

QY 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113

|||||

Db 61 SDFCLGCAAAPPPAPFRLLPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113

|||||

#### RESULT 14

US-09-700-590A-64

; Sequence 64, Application US/09700590A

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: TANG, Y. Tom

; APPLICANT: LAL, Preeti

; APPLICANT: HILLMAN, Jennifer L.

; APPLICANT: YUE, Henry

; APPLICANT: GUEGLER, Karl J.

; APPLICANT: CORLEY, Neil C.

; APPLICANT: BANDMAN, Olga

; APPLICANT: PATTERSON, Chandra

; APPLICANT: GORGONE, Gina A.

; APPLICANT: KASER, Matthew R.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: AU-YOUNG, Janice

; TITLE OF INVENTION: HUMAN TRANSMEMBRANE PROTEINS

; FILE REFERENCE: PF-0526 USN

; CURRENT APPLICATION NUMBER: US/09/700,590A

; CURRENT FILING DATE: 2001-04-16

; PRIOR APPLICATION NUMBER: 60/087,260

; PRIOR FILING DATE: 05-29-1998

; PRIOR APPLICATION NUMBER: 60/091,674

; PRIOR FILING DATE: 07-02-1998

; PRIOR APPLICATION NUMBER: 60/102,954

; PRIOR FILING DATE: 10-02-1998

; PRIOR APPLICATION NUMBER: 60/109,869

; PRIOR FILING DATE: 11-24-1998

; NUMBER OF SEQ ID NOS: 158

; SOFTWARE: PERL Program

; SEQ ID NO 64

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2454048
US-09-700-590A-64

Query Match      93.9%; Score 571; DB 21; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRAPH 60
   |||||
Db 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRAPH 60
   |||||

Qy 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRCRRRSSPPP 113
   |||||
Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRCRRRKFTTP 113
   |||||
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RESULT 15
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4
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Query Match      93.9%; Score 571; DB 21; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRAPH 60
   |||||
Db 1 MARGSLRRLRLLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRAPH 60
   |||||

Qy 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRCRRRSSPPP 113
   |||||
Db 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRCRRRKFTTP 113
   |||||
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Search completed: March 1, 2004, 16:48:23  
Job time : 182 secs

GenCore version 5.1.6  
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OMprotein - protein search, using sw model

Run on: March 1, 2004, 16:43:08 ; Search time 10 Seconds  
(without alignments)  
102.796 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLVLLGLWLA.....LSGFLVWRRCRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 99762 seqs, 9017151 residues

Total number of hits satisfying chosen parameters: 99762

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US05\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	84	13.8	152	6 US-10-767-701-33810	Sequence 33810, A
2	71	11.7	123	6 US-10-773-236-290	Sequence 290, App
3	67.5	11.1	368	6 US-10-667-762-10	Sequence 10, Appl
4	66.5	10.9	229	6 US-10-767-701-46659	Sequence 46659, A
5	66	10.9	1238	6 US-10-762-603-4	Sequence 4, Appli
6	65.5	10.8	271	6 US-10-417-375A-11	Sequence 11, Appl
7	65	10.7	189	6 US-10-767-701-43640	Sequence 43640, A
8	64.5	10.6	1417	6 US-10-767-471-1010	Sequence 1010, Ap
9	64.5	10.6	1421	6 US-10-767-471-1009	Sequence 1009, Ap
10	64.5	10.6	1557	6 US-10-767-471-1011	Sequence 1011, Ap
11	64.5	10.6	1557	6 US-10-767-471-1014	Sequence 1014, Ap
12	64.5	10.6	1587	6 US-10-767-471-1013	Sequence 1013, Ap
13	64.5	10.6	1587	6 US-10-767-471-1015	Sequence 1015, Ap
14	64.5	10.6	1664	6 US-10-767-471-1012	Sequence 1012, Ap
15	64	10.5	115	6 US-10-333-177-2	Sequence 2, Appli
16	63.5	10.4	126	6 US-10-767-701-60623	Sequence 60623, A
17	63.5	10.4	138	6 US-10-767-701-58471	Sequence 58471, A
18	63.5	10.4	150	6 US-10-767-701-54494	Sequence 54494, A
19	63.5	10.4	161	6 US-10-767-701-41647	Sequence 41647, A
20	63.5	10.4	193	6 US-10-767-701-33811	Sequence 33811, A
21	63.5	10.4	390	6 US-10-767-701-38237	Sequence 38237, A
22	63.5	10.4	476	1 PCT-US04-03417-8	Sequence 8, Appli
23	63.5	10.4	476	6 US-10-772-636-8	Sequence 8, Appli
24	62.5	10.3	283	6 US-10-451-467A-76	Sequence 76, Appl
25	62.5	10.3	355	6 US-10-767-701-37723	Sequence 37723, A
26	62.5	10.3	854	6 US-10-767-471-910	Sequence 910, App

27	62.5	10.3	1080	6 US-10-767-471-927	Sequence 927, App
28	62.5	10.3	1080	6 US-10-767-471-934	Sequence 934, App
29	62.5	10.3	1333	6 US-10-646-301A-12	Sequence 12, Appl
30	62.5	10.3	1333	6 US-10-663-208A-12	Sequence 12, Appl
31	62.5	10.3	2003	6 US-10-767-471-911	Sequence 911, App
32	62.5	10.3	2003	6 US-10-767-471-932	Sequence 932, App
33	62	10.2	108	6 US-10-767-701-50873	Sequence 50873, A
34	62	10.2	181	6 US-10-767-701-58367	Sequence 58367, A
35	61.5	10.1	216	6 US-10-767-701-38701	Sequence 38701, A
36	61	10.0	71	6 US-10-417-884A-4242	Sequence 4242, Ap
37	61	10.0	359	7 US-60-542-038-26	Sequence 26, Appl
38	60.5	10.0	168	6 US-10-767-701-35705	Sequence 35705, A
39	60.5	10.0	255	6 US-10-767-701-38374	Sequence 38374, A
40	60.5	10.0	1615	6 US-10-653-913-2	Sequence 2, Appli
41	60	9.9	113	6 US-10-767-701-31947	Sequence 31947, A
42	60	9.9	206	6 US-10-767-701-46607	Sequence 46607, A
43	60	9.9	228	6 US-10-767-701-42473	Sequence 42473, A
44	60	9.9	987	1 PCT-US04-02188-121	Sequence 121, App
45	60	9.9	987	6 US-10-764-425-121	Sequence 121, App

ALIGNMENTS

RESULT 1  
US-10-767-701-33810  
; Sequence 33810, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 33810  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C37651\_1.pep  
US-10-767-701-33810

Query Match	13.8%	Score 84;	DB 6;	Length 152;
Best Local Similarity	29.9%	Pred. No. 0.12;		
Matches	35;	Conservative	3;	Mismatches 25; Indels 54; Gaps 7;
QY	29	QAPGTAPCSR-----	GSSWSAD-LDKCMDASCARPHSDFC-----	64
Db	23	QAPGLAPAPRRRLLLCGGPDGAGCRWATDALAWCCRAPPCRLAP----	CPTALPALPG	78
QY	65	---LGCAAAPPAPFRLWPILGGALSLTFV-----	LGLLS---GFLVWRRCRR	106
Db	79	AGSLASCAAPP-----	GSASMTVVSRRPATALLLGLSSAPGPWAPRCRR	124

RESULT 2  
US-10-773-236-290  
; Sequence 290, Application US/10773236  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al.  
; TITLE OF INVENTION: 89 Human Secreted Proteins  
; FILE REFERENCE: PS751PI  
; CURRENT APPLICATION NUMBER: US/10/773,236  
; CURRENT FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/311,085  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,209  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: PCT/US02/25107  
; PRIOR FILING DATE: 2002-08-08

Query Match	11.1%;	Score 67.5;	DB 6;	Length 368;
Best Local Similarity	34.4%;	Pred. NO. 9.6;		
Matches 21; Conservative	2;	Mismatches 23;	Indels 15;	Gaps 2;
QY	65	LGCAAAPP-----	APFRLWPILGGALSLTFVLGLLSGFLVWRR	CRERSSP 111
			:	
Db	149	LGPPPPAPPAPARCSVLAGGLGPRPLWALLAFAL	LALLLGAYGGIFV--VARRAALRP	206
QY	112	P 112		
Db	207	P 207		

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RESULT 4
US-10-767-701-46659
; Sequence 46659, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46659
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C104_76.pep
US-10-767-701-46659

Query Match      10.9%; Score 66.5; DB 6; Length 229;
Best Local Similarity 28.7%; Pred. No. 7.7;
Matches 25; Conservative 8; Mismatches 29; Indels 25;

QY      39 GSSWSADLD-KCMDCASCR-----ARPHSDFCLGCAAAPPAFRLIWPIL---
      104 GAAWSTTLKFKVNESYSCRYMLGSKNADIHSDKLFNCTAEPEPSTTELLKRILLLE
DB

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Qy 90 FVLG 93  
Dp 1133 YEYG 1136

```
RESULT 9
US-10-767-471-1009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1009
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT FILING DATE: 2004-01-30
; CURRENT APPLICATION NUMBER: US/10/767,471
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1009
; LENGTH: 1421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1009

Query Match      10.6%; Score 64.5; DB 6; Length 1421;
Best Local Similarity 29.7%; Pred. No. 65;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

QY 36 CSRGSSWSADLDKCMDCASCRRPHSDFCCLGC-----AAAPPAPFRLLWPILGGALSLT 89
Db 1174 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRPPAYSPRP-----GGFGLP 1218

QY 90 FVLG 93
Db 1219 YEYG 1222

RESULT 10
US-10-767-471-1011
; Sequence 1011, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT FILING DATE: 2004-01-30
; CURRENT APPLICATION NUMBER: US/10/767,471
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1011
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1011

Query Match      10.6%; Score 64.5; DB 6; Length 1557;
Best Local Similarity 29.7%; Pred. No. 70;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

QY 36 CSRGSSWSADLDKCMDCASCRRPHSDFCCLGC-----AAAPPAPFRLLWPILGGALSLT 89
Db 1310 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRPPAYSPRP-----GGFGLP 1354

QY 90 FVLG 93
Db 1355 YEYG 1358

RESULT 11
US-10-767-471-1014
; Sequence 1014, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT FILING DATE: 2004-01-30
; CURRENT APPLICATION NUMBER: US/10/767,471
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1014

Query Match      10.6%; Score 64.5; DB 6; Length 1587;
Best Local Similarity 29.7%; Pred. No. 72;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;
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; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1014

Query Match      10.6%; Score 64.5; DB 6; Length 1557;
Best Local Similarity 29.7%; Pred. No. 70;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

QY 36 CSRGSSWSADLDKCMDCASCRRPHSDFCCLGC-----AAAPPAPFRLLWPILGGALSLT 89
Db 1310 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRPPAYSPRP-----GGFGLP 1354

QY 90 FVLG 93
Db 1355 YEYG 1358

RESULT 12
US-10-767-471-1013
; Sequence 1013, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT FILING DATE: 2004-01-30
; CURRENT APPLICATION NUMBER: US/10/767,471
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1013
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1013

Query Match      10.6%; Score 64.5; DB 6; Length 1587;
Best Local Similarity 29.7%; Pred. No. 72;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

QY 36 CSRGSSWSADLDKCMDCASCRRPHSDFCCLGC-----AAAPPAPFRLLWPILGGALSLT 89
Db 1340 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRPPAYSPRP-----GGFGLP 1384

QY 90 FVLG 93
Db 1385 YEYG 1388

RESULT 13
US-10-767-471-1015
; Sequence 1015, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT FILING DATE: 2004-01-30
; CURRENT APPLICATION NUMBER: US/10/767,471
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1015

Query Match      10.6%; Score 64.5; DB 6; Length 1587;
Best Local Similarity 29.7%; Pred. No. 72;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;
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QY 36 CSRGSSWSADLDKCMDCASCRRPHSDPCLGCG-----AAAPPAPFRLLWPILGGALSLT 89  
Db 1340 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1384

QY 90 FVLG 93  
Db 1385 YEYG 1388

RESULT 14  
US-10-767-471-1012  
; Sequence 1012, Application US/10767471  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001505  
; CURRENT APPLICATION NUMBER: US/10/767,471  
; CURRENT FILING DATE: 2004-01-30  
; NUMBER OF SEQ ID NOS: 50231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1012  
; LENGTH: 1664  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(1664)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-767-471-1012

Query Match 10.6%; Score 64.5; DB 6; Length 1664;  
Best Local Similarity 29.7%; Pred. No. 75;  
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

QY 36 CSRGSSWSADLDKCMDCASCRRPHSDPCLGCG-----AAAPPAPFRLLWPILGGALSLT 89  
Db 1335 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1379

QY 90 FVLG 93  
Db 1380 YEYG 1383

RESULT 15  
US-10-333-177-2  
; Sequence 2, Application US/10333177  
; GENERAL INFORMATION:  
; APPLICANT: Risoan, Marie-Clotilde  
; APPLICANT: Bridon, Jean-Michel  
; APPLICANT: Duhen, Thomas  
; APPLICANT: Briere, Francine  
; APPLICANT: Bates, Elizabeth  
; TITLE OF INVENTION: Type 2 Dendritic Cell Precursor Derived Coding Nucleic Acids and  
; TITLE OF INVENTION: Compositions and Methods  
; FILE REFERENCE: SF01190  
; CURRENT APPLICATION NUMBER: US/10/333,177  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: EP 00306087.8  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-333-177-2

Query Match 10.5%; Score 64; DB 6; Length 115;  
Best Local Similarity 30.8%; Pred. No. 7;  
Matches 16; Conservative 3; Mismatches 23; Indels 10; Gaps 2;

QY 29 QAP-----GTAPCSRGSWSADLDKCM-DCASCRRPHSDPCLGCAAA 70  
Db 4 QAPVVVVVTQPGVGPAPQNSNWOTGMCDCFSDCGVCLCGTFCFPCLGCQVA 55

Search completed: March 1, 2004, 16:48:48  
Job time : 13 secs





C;Function:  
A;Description: may be involved in flagellar assembly; may be involved in export of flagellin  
C;Superfamily: flagellar biosynthetic protein flip  
C;Keywords: flagellum; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-245/Product: probable export protein flip #status predicted <MAT>  
F;45-61/Domain: transmembrane #status predicted <TM1>  
F;89-105/Domain: transmembrane #status predicted <TM2>  
F;189-205/Domain: transmembrane #status predicted <TM3>  
F;212-228/Domain: transmembrane #status predicted <TM4>

Query Match 12.6%; Score 76.5; DB 2; Length 245;  
Best Local Similarity 30.8%; Pred. No. 4.3;  
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLLRLVLGLWLLRLSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRRP--- 59  
Db 1 MRRLLFLSLAGLW--LFSPAAAALPGLISQPLAGGQSWLSVQTLVFITSLTFLPAIL 58

QY 60 --HSDF-----CLGCAAAAPPAPFRLLPILGGALSFTVL 92  
Db 59 LMMTSFTRIIVFGLLRNALGTPSAPPNQV-----LLGLALFTFFI 100

RESULT 3  
AD0753  
flagellar biosynthetic protein Flip [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AD0753  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, R.; Davies, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi A  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AD0753  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-245 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD05727.1; PID:gl6503220; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY2187  
C;Superfamily: flagellar biosynthetic protein flip

Query Match 12.6%; Score 76.5; DB 2; Length 245;  
Best Local Similarity 30.8%; Pred. No. 4.3;  
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLLRLVLGLWLLRLSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRRP--- 59  
Db 1 MRRLLFLSLAGLW--LFSPAAAALPGLISQPLAGGQSWLSVQTLVFITSLTFLPAIL 58

QY 60 --HSDF-----CLGCAAAAPPAPFRLLPILGGALSFTVL 92  
Db 59 LMMTSFTRIIVFGLLRNALGTPSAPPNQV-----LLGLALFTFFI 100

RESULT 4  
B70939  
hypothetical protein Rv0246 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C;Accession: B70939  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70939  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-436 <COL>  
A;Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA17338.1; PID:el252444  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0246

Query Match 12.4%; Score 75.5; DB 2; Length 436;  
Best Local Similarity 23.0%; Pred. No. 8.4;  
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

QY 1 MARGSLRLRLRLVLGLWLLRLSVAGEQA--PGTAPCSRGS--WSADLDKCMDCASC 56  
Db 142 MPSTARARILLTEVGVGAALTAVVAATLSFVDPDQHPLSRNIHLWTAAVAMASAAICR 201

QY 57 ARPHSDFCLGCAAAAPPAPFRLW-----PILGG----- 84  
Db 202 ALPHR--IVPRVHAAPGLHKLTVYVGTARTNGWYRRYLLVQLVFGSVVLGSSFHISIRVA 259

QY 85 -----ALSLTFVLGSLGFLVWRRRCR 105  
Db 260 AVPGDQPDDEVAVVWLVFCVGLLGGIALWNRVR 291

RESULT 5  
T20910  
hypothetical protein ZK1010.9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C;Accession: T20910; T27646  
R;McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19345  
A;Accession: T20910  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-635 <WIL>  
A;Cross-references: EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9  
A;Experimental source: clone F14F7  
R;Gardner, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20398  
A;Accession: T27646  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-635 <WI2>  
A;Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9  
A;Experimental source: clone ZK1010  
C;Genetics:  
A;Gene: CESP:ZK1010.9  
A;Map position: 3  
A;Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3  
C;Superfamily: gamma-aminobutyric acid transporter

Query Match 12.4%; Score 75.5; DB 2; Length 635;  
Best Local Similarity 36.6%; Pred. No. 11;  
Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;

QY 31 PGTAPCSRGSWSADLDKCMDCASCRRAP--HSDFLG--CAAAPAPFRLLPILGGAL 86  
Db 92 PTTAYKNGGLSF--LIAYVVCGLFAVPAIHMEFALGQYAAKSPPAFRMRMPILGVG 148

QY 87 SLTFVLGGLSG 97  
Db 149 WMTCLVGAIG 159

RESULT 6  
B87353  
hypothetical protein CC0837 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus



A;Molecule type: DNA  
A;Residues: 1-346 <WHI>  
A;Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646000  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR2205  
A;Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;  
Best Local Similarity 28.8%; Pred. No. 13;  
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

QY 12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC---RAPHSD----FC 64

Db 87 LLVTCVGLGLV--TAGSASPTV-----MWVGALVAAFAGAVLATVWHLRPAAGSLFFVFA 138

QY 65 LGCAAA--PPAPFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 113

Db 139 VGTVGALPHAPLPALAVSGGAAALSVALGALGAHSTTRAPHELAAPPP 189

RESULT 11  
A55624  
fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 24-Nov-2003  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; MUID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin; EGF homology  
F;1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;  
Best Local Similarity 25.3%; Pred. No. 75;  
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36 CSRGSSWSADLDKCMD-----CASCRRPHS-----DFCLGC 67

Db 2040 CPEGFSWS\$GRRQCQLRMSYCAKFEKGKSSPKSRNHSKQECCKALKGEGWGPCELC 2099

QY 68 AAAPPAPFRLLWPILGGAL 86

Db 2100 PTEPDEAFRQICPFGSGII 2118

RESULT 12  
T36798  
probable transcription regulator soxR-like - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
C;Accession: T36798  
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21614  
A;Accession: T36798  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-175 <OLI>  
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18c  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SCI30A.18c

Query Match 11.7%; Score 71; DB 2; Length 175;

Best Local Similarity 29.0%; Pred. No. 11;  
Matches 29; Conservative 12; Mismatches 33; Indels 26; Gaps 5;  
QY 2 ARGSLRLLRLLV---LGLWLALLRSVAGEQAPGTAP-----CSRGSSWSADLDKCMDC 53  
Db 49 ARDALRRVAFVRAAQRVGIPLATIREALAEPLPEGRTPTEDDWARLSESWRSELDRIKQL 108  
QY 54 SCRARPHSDFCLGCAAAAPPAPFRLLWPILGGALSITFVL 92  
Db 109 N-RLRDHLTDCIGC-----GCLSLETQVL 131

RESULT 13  
E95850  
probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) mag  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C;Accession: E95850  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: E95850  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <KUR>  
A;Cross-references: GB:AL591985; PIDN:CAC48469.1; PID:g15139941; GSPDB:GN00167  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: SMB20069  
A;Genome: plasmid  
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;  
Best Local Similarity 26.4%; Pred. No. 26;  
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLWL-----ALLRSVAGEQA-PGTAPCSRGS-----SWSADLD 47

Db 322 LAIMVSGVWASGETGAVLSSAAFEALPG-----YGNVLVTISLAFATILGWAYYAE 376

QY 48 KCMDCASCRRPHSDFCLGCAAAAPPAPFRLLWPI---LGGALSITF 90

Db 377 KCW-----EYLIGTASA--IPFRIVTVAVFFGATLSLDF 409

RESULT 14  
I56545  
glypican precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 31-Jan-2000  
C;Accession: I56545; JCI281; PC1132  
R;Litwack, B.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.  
J. Neurosci. 14, 3713-3724, 1994  
A;Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-anc  
A;Reference number: I56545; MUID:94267529; PMID:8207484  
A;Accession: I56545  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-558 <RES>  
A;Cross-references: GB:L34067; NID:g506416; PIDN:AAA41251.1; PID:g506417  
R;Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.  
Biochem. Biophys. Res. Commun. 188, 395-401, 1992  
A;Title: Cloning of a major heparan sulfate proteoglycan from brain and identification as

A;Reference number: JCI1281; MUID:93038690; PMID:1417860  
A;Accession: JCI1281  
A;Molecule type: mRNA  
A;Residues: 1-20,'T','Y',22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>  
A;Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425  
A;Experimental source: brain  
A;Accession: PC1132  
A;Molecule type: protein  
A;Residues: 24-55;424-445 <KA2>  
C;Superfamily: glypican  
C;Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; heparan  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-530/Product: glypican #status predicted <MAT>  
F;531-558/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;55,486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
F;79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;399,512/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F;530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 11.5%; Score 70; DB 2; Length 558;  
Best Local Similarity 37.7%; Pred. No. 33;  
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC 64  
Db 221 RSFVQGLGVASDVRKVA--QVPLAPECRA-----VMKLVYCAHCRGVPGARPCPDYC 272

QY 65 ----LGCAA 69  
Db 273 RNVLKGCLA 281

RESULT 15  
D75330  
Probable beta-lactamase - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C;Accession: D75330  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: D75330  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-424 <WHI>  
A;Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645977  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR1985  
A;Map position: 1

Query Match 11.4%; Score 69.5; DB 2; Length 424;  
Best Local Similarity 29.7%; Pred. No. 30;  
Matches 30; Conservative 11; Mismatches 35; Indels 25; Gaps 4;

QY 3 RGSLLRRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----- 57  
Db 2 RGTIRLTLLALLLG---AGINACRNREAQDTAPPAAAAQSQAAPRKAASASSPAPTATE 58

QY 58 ----RPHSDFCLGCAA-----PPAPFRLWPILGGALS 88  
Db 59 PAVSAPAAADGCLPAAPAVTQAPRPPQP-----LSGRLLGL 92



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:37:03 ; Search time 17 Seconds  
(without alignments)  
349.176 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLLRLVLGLWLA.....LSGFLVWRRRCRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	93.9	129	1 FN14 HUMAN	Q9np84 homo sapien
2	445	73.2	129	1 FN14 MOUSE	Q9cr75 m tumor nec
3	87	14.3	184	1 T13C_HUMAN	Q96rj3 homo sapien
4	78	12.8	448	1 FBL5 RAT	Q9wvh8 rattus norv
5	77	12.7	448	1 FBL5_MOUSE	Q9wvh9 mus musculu
6	76.5	12.6	245	1 FLIP_SALTY	P54700 salmonella
7	74	12.2	548	1 LGI3_MOUSE	Q8k406 mus musculu
8	73.5	12.1	81	1 PORD METH	P56815 methanobact
9	72	11.8	1278	1 NPCL1_HUMAN	O15118 homo sapien
10	72	11.8	2871	1 FBN1_MOUSE	O61554 mus musculu
11	70	11.5	301	1 CTF5_HUMAN	Q9uaj2 homo sapien
12	70	11.5	443	1 FBL4_MOUSE	Q9wvj9 mus musculu
13	70	11.5	558	1 GPC1 RAT	P35053 rattus norv
14	69.5	11.4	495	1 MLP2 DROME	Q24400 drosophila
15	69	11.3	180	1 PTTG_HUMAN	P53801 homo sapien
16	69	11.3	314	1 TRI2_HUMAN	Q14140 homo sapien
17	69	11.3	324	1 TNR6 RAT	Q63199 rattus norv
18	68.5	11.3	205	1 GSCL_HUMAN	O15499 homo sapien
19	68.5	11.3	431	1 YG84 METH	O27719 methanobact
20	67.5	11.1	368	1 GP62_HUMAN	Q9bzj7 homo sapien
21	67.5	11.1	1008	1 VGLM UUK	P09613 uukuniemi v
22	67.5	11.1	1013	1 EPA5_CHICK	P54755 gallus gall
23	67	11.0	279	1 CXEL1_HUMAN	Q8nfk1 homo sapien
24	67	11.0	319	1 BST1 RAT	Q63072 rattus norv
25	67	11.0	386	1 HXAD_MOUSE	Q62424 mus musculu
26	67	11.0	1005	1 EPA5 RAT	P54757 rattus norv
27	67	11.0	2871	1 FBN1_PIG	Q9tv36 sus scrofa
28	66.5	10.9	443	1 FBL4 CRIGR	O55058 cricetus
29	66	10.9	394	1 Y6B9_PSEAE	P42514 pseudomonas
30	66	10.9	992	1 POLS_RUBVM	P08563 rubella vir
31	66	10.9	1238	1 JAG2_HUMAN	Q9y219 homo sapien
32	66	10.9	2318	1 NTC3_MOUSE	Q61982 mus musculu
33	66	10.9	2319	1 NTC3 RAT	Q9r172 rattus norv

34	65.5	10.8	245	1 FLIP_ECOLI	P33133 escherichia
35	65.5	10.8	2321	1 NTC3_HUMAN	Q9um47 homo sapien
36	65	10.7	453	1 HRA3_HUMAN	P83110 homo sapien
37	65	10.7	1014	1 EPB6_MOUSE	O08644 mus musculu
38	65	10.7	1445	1 PTPG_HUMAN	P23470 homo sapien
39	64.5	10.6	112	1 PLA8_MOUSE	Q9ji48 mus musculu
40	64.5	10.6	123	1 VST1_HEVME	Q03499 hepatitis e
41	64.5	10.6	300	1 TR6B_HUMAN	O95407 homo sapien
42	64.5	10.6	443	1 FBL4_HUMAN	O95967 homo sapien
43	64	10.5	115	1 PLA8_HUMAN	Q9nzf1 homo sapien
44	64	10.5	1210	1 EGFR_MOUSE	Q01279 mus musculu
45	64	10.5	1227	1 B3A3_MOUSE	P16283 mus musculu

ALIGNMENTS

RESULT 1  
FN14\_HUMAN  
ID FN14\_HUMAN STANDARD; PRT; 129 AA.  
AC Q9NP84; Q9HCS0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
DE (Fibroblast growth factor-inducible immediate-early response protein  
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).  
GN TNFRSF12A OR FN14.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Placenta;  
RX MEDLINE=20216634; PubMed=10751351;  
RA Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,  
RA Testa J.R., Peifley K.A., Winkles J.A.;  
RA "The Fn14 immediate-early response gene is induced during liver  
RA regeneration and highly expressed in both human and murine  
RA hepatocellular carcinoma.";  
RL Am. J. Pathol. 156:1253-1261(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Tanaka S., Sugimachi K.;  
RA "Human homologue of Fn14.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Uterus;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION.

```
RX MEDLINE=21585797; PubMed=11728344;
RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RT "A novel TNF receptor family member binds TWEAK and is implicated in
RT angiogenesis."
RL Immunity 15:837-846(2001).
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_00519;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC -!- INDUCTION: By FGF-1 and phorbol ester.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
CC -----
EMBL; AF1911148; AAF69108.1; -
DR EMBL; AB035480; BAA94792.1; -
DR EMBL; AB035481; BAB17850.1; -
DR EMBL; BC002718; AAH02718.1; -
DR Genew; HGNC:18152; TNFRSF12A.
DR MIM; 605914; -
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007275; P:development; TAS.
DR InterPro; IPR001368; TNFR c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;
KW Alternative splicing;
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 129 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER FN14.
FT DOMAIN 28 80 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 81 101 POTENTIAL.
FT DOMAIN 102 129 CYTOPLASMIC (POTENTIAL).
FT REPEAT 36 67 TNFR-CYS (ATYPICAL).
FT DISULFID 36 49 POTENTIAL.
FT DISULFID 52 67 POTENTIAL.
FT VARSPLIC 33 67 Missing (in isoform 2).
FT /FTId=VSP_006519.
SQ SEQUENCE 129 AA; 13911 MW; BF3FDFB9C1E1C448 CRC64;
Query Match 93.9%; Score 571; DB 1; Length 129;
Best Local Similarity 94.7%; Pred. NO. 2.8e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Dd 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRCRRRSSPPP 113
Dd 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRCRRRKFTTP 113
, RESULT 2
```

```
FN14 MOUSE
ID FN14 MOUSE STANDARD; PRT; 129 AA.
AC Q9CR75; Q9QZM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member Fn14 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)
DE (Tweak-receptor) (TweakR).
DE TNFRSF12A OR FN14 OR FGFRP2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Fibroblast;
RX MEDLINE=20020297; PubMed=10551889;
RA Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,
RA Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Richards C.M., Winkles J.A.;
RA "The mitogen-inducible Fn14 gene encodes a type I transmembrane
RT protein that modulates fibroblast adhesion and migration.";
RL J. Biol. Chem. 274:33166-33176(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK (By similarity). Weak inducer
CC of apoptosis in some cell types. Promotes angiogenesis and the
CC proliferation of endothelial cells. May modulate cellular adhesion
CC to matrix proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine,
CC kidney, liver, lung and skin, and in adult heart and ovary.
CC Intermediate expression in adult kidney, lung and skin.
CC -!- INDUCTION: By FGF-1.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
CC -----
CC EMBL; AF156164; AAF07882.1; -.
CC EMBL; AK005530; BAB24101.1; -.
CC EMBL; AK005382; BAB23989.1; -.
CC EMBL; BC025860; AAH25860.1; -.
CC MGD; MGI:1351484; Tnf12a.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0007155; P:cell adhesion; IDA.
CC GO; GO:0006931; P:substrate-bound cell migration, cell attach. .; IDA.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
CC PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
CC Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal.
CC SIGNAL 1 27 POTENTIAL.
CC CHAIN 28 129 TUMOR NECROSIS FACTOR RECEPTOR
CC
CC DOMAIN 28 80 SUPERFAMILY MEMBER FN14.
CC TRANSMEM 81 101 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 102 129 POTENTIAL.
CC REPEAT 36 67 CYTOPLASMIC (POTENTIAL).
CC DISULFID 36 49 TNFR-CYS (ATYPICAL).
CC DISULFID 52 67 POTENTIAL.
CC CONFLICT 3 4 SA -> PG (IN REF. 1).
CC SEQUENCE 129 AA; 13641 MW; 1665C68B4D9A9253 CRC64;
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CC Query Match 73.2%; Score 445; DB 1; Length 129;
CC Best Local Similarity 74.3%; Pred. No. 3.6e-36;
CC Matches 84; Conservative 6; Mismatches 23; Indels 0; Gaps 0;
CC
CC QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRPH 60
CC Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC 1 MASAWPSLPQILVGLVLMRAAGEQAPGTSPCSSGSSWSADLCKMDCASCRRPH 60
CC
CC QY 61 SDFCLGCAAAPPAFFRLLPILGGALSITFVLGSLVWRRCRERSPPPP 113
CC Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC 61 SDFCLGCAAAPPAFFRLLPILGGALSILVILVSSFLVWRRCRREKFTTP 113
CC
CC RESULT 3
CC T13C_HUMAN
CC ID T13C_HUMAN STANDARD; PRT; 184 AA.
CC AC Q96RJ3;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tumor necrosis factor receptor superfamily member 13C (B cell-
CC activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor
CC 3).
CC GN TNFSF13C OR BAFFR OR BR3.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
```

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RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA Ambrose C.;
RA "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RX FUNCTION.
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552(2001).
CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BlyS.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96RJ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96RJ3-2; Sequence=VSP_006505;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC in resting B-cells. Detected at lower levels in activated B-cells,
CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
CC -----
CC EMBL; AF373846; AAK91826.1; -.
CC PDB; 1MPV; 30-OCT-02.
CC Genew; HGNC:17755; TNFRSF13C.
CC MIM; 606269; -.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
CC PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
CC Receptor; Immune response; Signal-anchor; Transmembrane;
CC Alternative splicing; 3D-structure.
CC DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 79 99 SIGNAL-ANCHOR
CC (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
CC DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).
CC REPEAT 18 35 TNFR-CYS (PARTIAL).
CC DISULFID 19 32 BY SIMILARITY.
CC DISULFID 24 35 BY SIMILARITY.
CC VARSPLIC 143 143 P -> PA (in isoform 2).
CC SEQUENCE 184 AA; 18863 MW; F2BFB98099A27138 CRC64;
CC
CC Query Match 14.3%; Score 87; DB 1; Length 184;
CC Best Local Similarity 27.0%; Pred. No. 0.13;
CC Matches 34; Conservative 11; Mismatches 41; Indels 40; Gaps 6;
CC
CC QY 23 RSVAGEQAPGTAPCSRGSWSADLCKMDCASCRA-RHSDFCGLCAAAPPAPFRLWP- 80
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 6 RSLRGRDAPAPTPTCPVPAECFDLLVRHCVACGLLRTPRKP-----AGASSAPRTALQPO 60
CC
CC QY 81 -----ILGGA---LSLTFVLGL-LSGFLVWRRCR-----E 107
CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 61 ESVGAGAGEAALPLPGLLFGAPALLGLALVLAFLVGLVSWRRRQRRLRGASSAEAPDGD 120
```









KW Protein transport; Signal; Complete proteome.  
FT SIGNAL 1 21  
FT CHAIN 22 245 FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.  
FT TRANSMEM 45 65 POTENTIAL.  
FT TRANSMEM 88 108 POTENTIAL.  
FT TRANSMEM 185 205 POTENTIAL.  
FT TRANSMEM 209 229 POTENTIAL.  
SQ SEQUENCE 245 AA; 26787 MW; C9A4241F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 1; Length 245;  
Best Local Similarity 30.8%; Pred. No. 1.8;  
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLLRLVLGLWLLRLRSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRRP--- 59  
Db 1 MRRLFLSLAGLW--LFSPAAAQLPGLISQPLAGGQSWLSVQTLVFITSLTFLPAIL 58

QY 60 --HSDF-----CLGCAAAPPPAPFRLLWPILGGALSLTFVL 92  
Db 59 LMMTSFTRIIVFGLLRNALGTPSPAPNOV-----LLGLALFLTFFI 100

RESULT 7  
LGI3\_MOUSE  
ID LGI3\_MOUSE STANDARD; PRT; 548 AA.  
AC Q8K406;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Leucine-rich repeat LGI family member 3 precursor (Leucine-rich  
DE glioma-inactivated protein 3) (Leubrin).  
GN LGI3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Brain;  
RA Yun H.-Y., Lee S.E.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- SIMILARITY: Contains 6 EAR repeats.  
CC -!- SIMILARITY: Contains 5 leucine-rich (LRR) repeats.  
CC -----  
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CC -----  
DR EMBL; AF515590; AAM55219.1; -;  
DR EMBL; AY174077; AAO19739.1; -;  
DR EMBL; AK049831; BAC33943.1; -;  
DR EMBL; BC055315; AAH55315.1; -;  
DR EMBL; BC061460; AAH61460.1; -;  
DR MGD; MGI:2182619; Lgi3.  
DR InterPro; IPR009039; EAR.  
DR InterPro; IPR005492; EPTP.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR003591; LRR\_type.  
DR Pfam; PF03736; EPTP; 2.  
DR Pfam; PF00560; LRR; 3.  
DR Pfam; PF01463; LRRCT; 1.  
DR SMART; SM00369; LRR\_TYP; 3.  
DR SMART; SM00082; LRRCT; 1.  
DR PROSITE; PS00912; EAR; 6.  
KW Repeat; Leucine-rich repeat; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 548 LEUCINE-RICH REPEAT LGI FAMILY MEMBER 3.  
FT REPEAT 63 86 LRR 1.  
FT REPEAT 87 110 LRR 2.  
FT REPEAT 112 134 LRR 3.  
FT REPEAT 135 158 LRR 4.  
FT REPEAT 160 183 LRR 5.  
FT REPEAT 221 264 EAR 1.  
FT REPEAT 267 310 EAR 2.  
FT REPEAT 313 361 EAR 3.  
FT REPEAT 362 406 EAR 4.  
FT REPEAT 409 453 EAR 5.  
FT REPEAT 454 497 EAR 6.  
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 548 AA; 61817 MW; 2DB303936354B958 CRC64;

Query Match 12.2%; Score 74; DB 1; Length 548;

Best Local Similarity 40.4%; Pred. No. 6.4; Matches 21; Conservative 5; Mismatches 24; Indels 2; Gaps 1;

```
QY 3 RGSRLRLRLLLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCAS 54
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 RGPGRLLVLTGLFCLML--QVSAKRPPKTPPCPPSCSTRDTAFCDVDSK 57
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 8

```
PORD_METHTH STANDARD; PRT; 81 AA.
AC P56815;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit porD (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
GN POR OR MTH1740.1.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
CC -!- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
CC -!- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
CC PORC AND POR. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
-----
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-----
CC EMBL; AE000929; AAB86210.1; ALT_INIT.
CC HSSP; P00195; 1CLF.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC Pfam; PF00037; fer4; 2.
CC PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
KW Complete proteome.
FT METAL 34 34 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
FT METAL 37 37 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
FT METAL 40 40 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
FT METAL 44 44 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
FT METAL 60 60 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
FT METAL 63 63 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
FT METAL 66 66 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
FT METAL 70 70 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
SQ SEQUENCE 81 AA; 9121 MW; 219A9CCAE8A41604 CRC64;
```

## Query Match

Best Local Similarity 12.1%; Score 73.5; DB 1; Length 81;  
Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;

```
QY 31 PGTAPCSRSGSSWSA-----DLDKCMDCASRA-----RPHS---DFCLGCA-AAPPA 73
||| :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 11 PGSTVKNKTSWRTFKPVLDDKDKIDCDNCILFCEGCINREHEIDYDYCKGGGICAEKC 70
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 PFRLL 78
| :|
Db 71 PVKAI 75
```

## RESULT 9

```
NPC1_HUMAN
ID NPC1_HUMAN STANDARD; PRT; 1278 AA.
AC O15118; Q9P130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Niemann-Pick C1 protein precursor.
GN NPC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS NPC1.
RX MEDLINE=97362323; PubMed=9211849;
RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
RA Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,
RA Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,
RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
RA Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,
RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
RT homeostasis.";
RL Science 277:228-231(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=99355599; PubMed=10425213;
RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
RA Carstea E.D.;
RT "The genomic organization and polymorphism analysis of the human
RT Niemann-Pick C1 gene.";
RL Biochem. Biophys. Res. Commun. 261:493-498(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623216; PubMed=11754101;
RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
RT "NPC1: Complete genomic sequence, mutation analysis, and
RT characterization of haplotypes.";
RL Hum. Mutat. 19:30-38(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99128318; PubMed=9927649;
RA Watarai H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,
RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
RT lysosomal targeting in cholesterol mobilization.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
RN [5]
RP VARIANT NPD TRP-992.
RX MEDLINE=98299797; PubMed=9634529;
RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
RA Byers D.M., Dobson M.J., Neumann P.E.;
RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
RT G3097-->T transversion in NPC1.";
RL Am. J. Hum. Genet. 63:52-54(1998).
RN [6]
RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;
RP THR-1061 AND VAL-1213.
RX MEDLINE=99452586; PubMed=10521290;
```



RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,  
RA Neumann P.E.;  
RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich  
RT domain.";  
RL Am. J. Hum. Genet. 65:1252-1260(1999).  
RN [7]  
RP VARIANT NPC1 THR-1061.  
RX MEDLINE=99452593; PubMed=10521297;  
RA Millat G., Marçais C., Rafi M.A., Yamamoto T., Morris J.A.,  
RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;  
RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant  
RT allele in patients of Western European descent and correlates with a  
RT classic juvenile phenotype.";  
RL Am. J. Hum. Genet. 65:1321-1329(1999).  
RN [8]  
RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.  
RX MEDLINE=99408226; PubMed=10480349;  
RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,  
RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,  
RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,  
RA Ohno K.;  
RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease  
RT type C";  
RL Hum. Genet. 105:10-16(1999).  
RN [9]  
RP VARIANTS NPC1 GLN-958 AND ALA-1007.  
RX MEDLINE=21313111; PubMed=11349231;  
RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,  
RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;  
RT "Niemann-Pick C variant detection by altered sphingolipid trafficking  
RT and correlation with mutations within a specific domain of NPC1.";  
RL Am. J. Hum. Genet. 68:1361-1372(2001).  
RN [10]  
RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.  
RX MEDLINE=21313105; PubMed=11333381;  
RA Millat G., Marçais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,  
RA Wenger D.A., Ohno K., Vanier M.T.;  
RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels  
RT of NPC1 protein, and phenotypes emphasize the functional significance  
RT of the putative sterol-sensing domain and of the cysteine-rich  
RT luminal loop.";  
RL Am. J. Hum. Genet. 68:1373-1385(2001).  
RN [11]  
RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.  
RX MEDLINE=21372069; PubMed=11479732;  
RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,  
RA Millat G.;  
RT "Niemann-Pick type C disease: NPC1 mutations associated with severe  
RT and mild cellular cholesterol trafficking alterations.";  
RL Hum. Genet. 109:24-32(2001).  
CC -!- FUNCTION: Involved in the intracellular trafficking of  
CC cholesterol. May play a role in vesicular trafficking in glia, a  
CC process that may be crucial for maintaining the structural and  
CC functional integrity of nerve terminals.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late  
CC endosomes and lysosomes.  
CC -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain  
CC containing a di-leucine motif necessary for lysosomal targeting  
CC are critical for mobilization of cholesterol from lysosomes.  
CC -!- PTM: Glycosylated.  
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
CC type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid  
CC storage disorder, which affects particularly the brain, liver and  
CC spleen, and which is characterized by lysosomal accumulation of  
CC low density lipoprotein derived cholesterol. Clinical features  
CC include variable hepatosplenomegaly and severe progressive  
CC neurological dysfunction such as ataxia, dystonia and dementia.  
CC The age of onset can vary from infancy to late adulthood.  
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
CC type D (NPD) [MIM:257250]; also known as Niemann-Pick disease  
CC without sphingomyelinase deficiency, or Nova Scotian type. Because  
CC of evidence from biochemical changes, lack of complementation, and  
CC linkage mapping to the same chromosome site, NPD and NPC1 are

CC considered to be allelic disorders.  
CC -!- SIMILARITY: Belongs to the patched family.  
CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.  
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CC -----  
CC EMBL; AF002020; AAB63982.1; - -  
DR EMBL; AF157379; AAD48006.1; - -  
DR EMBL; AF157365; AAD48006.1; JOINED.  
DR EMBL; AF157366; AAD48006.1; JOINED.  
DR EMBL; AF157367; AAD48006.1; JOINED.  
DR EMBL; AF157368; AAD48006.1; JOINED.  
DR EMBL; AF157369; AAD48006.1; JOINED.  
DR EMBL; AF157370; AAD48006.1; JOINED.  
DR EMBL; AF157371; AAD48006.1; JOINED.  
DR EMBL; AF157372; AAD48006.1; JOINED.  
DR EMBL; AF157373; AAD48006.1; JOINED.  
DR EMBL; AF157374; AAD48006.1; JOINED.  
DR EMBL; AF157375; AAD48006.1; JOINED.  
DR EMBL; AF157376; AAD48006.1; JOINED.  
DR EMBL; AF157377; AAD48006.1; JOINED.  
DR EMBL; AF157378; AAD48006.1; JOINED.  
DR EMBL; AF338230; AAK25791.1; - -  
DR EMBL; AF123046; AAF28875.1; - -  
DR EMBL; AF123045; AAF28875.1; JOINED.  
DR Genew; HGNC:7897; NPC1.  
DR MIM; 607623; - -  
DR MIM; 257220; - -  
DR MIM; 257250; - -  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005764; C:lysosome; TAS.  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0005478; F:intracellular transporter activity; TAS.  
DR GO; GO:0015248; F:sterol transporter activity; TAS.  
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.  
DR InterPro; IPR004765; NP\_C\_type.  
DR InterPro; IPR003392; Patched.  
DR InterPro; IPR000731; SSD STM.  
DR Pfam; PF02460; Patched; I.  
DR TIGRFAMs; TIGR00917; 2A060601; 1.  
DR PROSITE; PS50156; SSD; 1.  
DR Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;  
KW Disease mutation.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 1278 NIEMANN-PICK C1 PROTEIN.  
FT TRANSMEM 270 290 POTENTIAL.  
FT TRANSMEM 351 371 POTENTIAL.  
FT TRANSMEM 622 642 POTENTIAL.  
FT TRANSMEM 655 675 POTENTIAL.  
FT TRANSMEM 678 698 POTENTIAL.  
FT TRANSMEM 760 780 POTENTIAL.  
FT TRANSMEM 833 853 POTENTIAL.  
FT TRANSMEM 1099 1119 POTENTIAL.  
FT TRANSMEM 1125 1145 POTENTIAL.  
FT TRANSMEM 1196 1216 POTENTIAL.  
FT TRANSMEM 1228 1248 POTENTIAL.  
FT DOMAIN 249 259 POLY-PRO.  
FT DOMAIN 620 785 SSD.  
FT SITE 1275 1278 DI-LEUCINE MOTIF.  
FT CARBOHYD 70 N-LINKED (GLCNAC. . .) (POTENTIAL).  
Query Match 11.8%; Score 72; DB 1; Length 1278;  
Best Local Similarity 31.4%; Pred. No. 22;  
Matches 27; Conservative 8; Mismatches 17; Indels 34; Gaps 7;  
QY 33 TAPCSRGSSWSADLDKCMDCA-SCRRAPSHSDFCLGCAAPAPFRLLWPILG-----GAL 86  
||||| :||:|:| :||| :|||





FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.
FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
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FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
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FT	DISULFID	750	763	BY SIMILARITY.
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FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
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FT	DISULFID	832	845	BY SIMILARITY.
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FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
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FT	DISULFID	1291	1305	BY SIMILARITY.
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FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
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FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
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FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.
Query Match 11.8%; Score 72; DB 1; Length 2871;				
Best Local Similarity 25.3%; Pred. No. 46;				
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;				
QY	36	CSRGSSWSADLDKCMD-----CASCRRPHS-----	DFCLGC	67
Db	2040	CPEGFSWSSGRRQCQDLRMSVCYAKFEGGKCSSPKSRNHSKQECCKALKGEGWGPCELC		2099
QY	68	AAAPPAPRLLWPILGGAL	86	

Db	2100	PTEPDEAFRQICPFGSGII	2118	
RESULT 11				
CTF5_HUMAN		STANDARD;	PRT;	301 AA.
AC	Q9UJA2;			
DT	10-OCT-2003	(Rel. 42, Created)		
DT	10-OCT-2003	(Rel. 42, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Protein C20orf155.			
GN	C20ORF155.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver cancer;			
RA	Cheng Z., Gao G., Peng Y., Ren S., Chen Z., Han Z.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslaiho M.H., Lerversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			
RT	"The DNA sequence and comparative analysis of human chromosome 20.";			
RL	Nature 414:865-871(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase  
CC class-I family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF241784; AAG44472.1; -.  
DR EMBL; AL035461; CAB55278.1; -.  
DR EMBL; BC015333; AAI15333.1; -.  
DR Genew; HGNC:16148; C20orf155.  
DR InterPro; IPR000462; CDP-OH\_P\_transf.  
DR Pfam; PF01066; CDP-OH\_P\_transf; 1.  
DR PROSITE; PS00379; CDP\_ALCOHOL\_P\_TRANSF; FALSE\_NEG.  
KW Transferase; Transmembrane.  
FT TRANSMEM 179 199 POTENTIAL.  
FT TRANSMEM 250 270 POTENTIAL.  
FT TRANSMEM 272 292 POTENTIAL.  
SQ SEQUENCE 301 AA; 32593 MW; 15CD406D29D3C405 CRC64;  
  
\* Query Match 11.5%; Score 70; DB 1; Length 301;  
Best Local Similarity 22.6%; Pred. No. 8.9;  
Matches 36; Conservative 13; Mismatches 42; Indels 68; Gaps 9;  
  
QY 16 GLWLALLRSVAGEQAPGTAPCSRGSSWS--ADLDKCMDCAS--CRARP-----H 60  
Db 9 GSWGA-LRGAA--WAPGTRPSKRRACWALLPPVPCCLGCLAERWRLRPAALGLRLPGIGQ:65  
  
QY 61 SDFCLGCAAAPAP-----FRLW-----PILG 83  
Db 66 RNHCSGAGKAAAPPAAGAGAAEAPGGQGWGPASTPSLYENPWTIPNMLSMTRIGLAPVLG 125  
  
QY 84 -----GALSILTFVLGLLSGFLVWRRCRRSS 110  
Db 126 YLIIIEEDFNIALGVFALAGLTDLDDGFIA-RNWANQRSA 163  
  
RESULT 12  
FBL4 MOUSE STANDARD; PRT; 443 AA.  
AC Q9WVJ9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE EGF-containing fibulin-like extracellular matrix protein 2 precursor  
DE (Fibulin-4) (FBLN-4) (Mutant p53 binding protein 1).  
GN EFEMP2 OR FBLN4 OR MBP1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=99308589; PubMed=10380882;  
RA Gallagher W.M., Argentin M., Sierra V., Bracco L., Debussche L.,  
RA Conseiller E.;  
RT "MBP1: a novel mutant p53-specific protein partner with oncogenic  
RT properties.";  
RL Oncogene 18:3608-3616(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBUNIT: Binds preferentially to p53 mutants.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the fibulin family.  
CC -!- SIMILARITY: Contains 6 EGF-like domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF104223; AAD45219.1; -.  
DR EMBL; BC012269; AAI12269.1; -.  
DR HSSP; P00736; IAPQ.  
DR MGD; MGI:1891209; Efemp2.  
DR InterPro; IPR000152; Asx\_hydroxyl\_s.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001491; Thrbomoduln.  
DR Pfam; PF00008; EGF; 3.  
DR PRINTS; PR00907; THRBOMODULN.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS50026; EGF\_3; 4.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR  
FT MATRIX PROTEIN 2.  
FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.  
FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
FT DISULFID 127 140 BY SIMILARITY.  
FT DISULFID 134 149 BY SIMILARITY.  
FT DISULFID 151 162 BY SIMILARITY.  
FT DISULFID 168 177 BY SIMILARITY.  
FT DISULFID 173 186 BY SIMILARITY.  
FT DISULFID 188 201 BY SIMILARITY.  
FT DISULFID 207 217 BY SIMILARITY.  
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FT DISULFID 287 300 BY SIMILARITY.  
FT DISULFID 294 309 BY SIMILARITY.  
FT DISULFID 315 327 BY SIMILARITY.



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FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 443 AA; 49425 MW; 4969C0328A23DD88 CRC64;

Query Match 11.5%; Score 70; DB 1; Length 443;
Best Local Similarity 27.3%; Pred. No. 13;
Matches 24; Conservative 5; Mismatches 33; Indels 26; Gaps 3;

QY 13 LVIGLWLAIRSVAGEQAP-----GTAPCSRGSSWSADLDKCMDCASCRRPHS----- 61
Db 12 LLLWAFLLLLGGAASPDPEEPDSYTECTDGYEWDADSQHCRDVNECLTIPEACKGEMKC 71

QY 62 -----DFCLGCAA-----PPAP 74
Db 72 INHYGYLCLPRSAAVISDLHGEGPPPP 99

RESULT 13
GPC1_RAT
ID GPC1_RAT STANDARD; PRT; 558 AA.
AC P35053;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glypican-1 precursor (HSPG M12).
GN GPC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
RC TISSUE=Brain;
RX MEDLINE=93038690; PubMed=1417860;
RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
RT "Cloning of a major heparan sulfate proteoglycan from brain and
RT identification as the rat form of glypican."
RL Biochem. Biophys. Res. Commun. 188:395-401(1992).
RN [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
RC STRAIN=New England Deaconess Hospital;
RX MEDLINE=94267529; PubMed=8207484;
RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;
RT "Neuronal expression of glypican, a cell-surface
RT glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
RT in the adult rat nervous system."
RL J. Neurosci. 14:3713-3724(1994).
CC -!- FUNCTION: Cell surface proteoglycan that bears heparan sulfate.
CC May play an important role in the trophic and injury responses of
CC neurons.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Nervous system.
CC -!- PTM: This cell-associated glypican is further processed to give
CC rise to a medium-released species.
CC -!- SIMILARITY: Belongs to the glypican family.
CC -----
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CC -----
DR EMBL; L02896; AAA86439.1; -.
DR EMBL; L34067; AAA41251.1; -.
DR PIR; I56545; I56545.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001863; Glypican.
DR Pfam; PF01153; Glypican; 1.
DR PROSITE; PS01207; GLYPICAN; 1.
KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
KW Extracellular matrix; Lipoprotein.
```

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FT SIGNAL 1 23 GLYPICAN-1.
FT CHAIN 24 530 REMOVED IN MATURE FORM (POTENTIAL).
FT PROPEP 531 558 GPI-anchor amidated serine (POTENTIAL).
FT LIPID 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 486 486 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 488 488 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 490 490 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CONFLICT 21 21 T -> A (IN REF. 2).
FT CONFLICT 312 312 Y -> N (IN REF. 2).
FT CONFLICT 362 362 A -> G (IN REF. 2).
FT CONFLICT 437 437 I -> G (IN REF. 2; AA SEQUENCE).
FT CONFLICT 443 443 E -> D (IN REF. 2; AA SEQUENCE).
FT CONFLICT 515 515 I -> T (IN REF. 2).
SQ SEQUENCE 558 AA; 61734 MW; E2878A854B9A1D7F CRC64;

Query Match 11.5%; Score 70; DB 1; Length 558;
Best Local Similarity 37.7%; Pred. No. 16;
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC-----ARPHSDFC 64
Db 221 RSFVQGLGVASDVVRKVA--QVPLAPECSPA-----VMKLVYCAHCRGVPGARPCPDYC 272

QY 65 ----LGCAA 69
Db 273 RNVLKGCLA 281

RESULT 14
MLP2_DROME
ID MLP2_DROME STANDARD; PRT; 495 AA.
AC Q24400; Q9VI62;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscle LIM protein MLP84B.
GN LIM3 OR MLP84B OR CGI0699.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96387325; PubMed=8794860;
RA Stronach B.E., Siegrist S.E., Beckerle M.C.;
RT "Two muscle-specific LIM proteins in Drosophila."
RL J. Cell Biol. 134:1179-1195(1996).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=99326429; PubMed=10397768;
RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;
RT "Muscle LIM proteins are associated with muscle sarcomeres and require
RL dMEF2 for their expression during Drosophila myogenesis."
RN Mol. Biol. Cell 10:2329-2342(1999).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
```







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:19 ; Search time 40 Seconds  
(without alignments)  
899.227 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLLLVLGLWLA.....LSGFLVWRRRCRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	453	74.5	129	11 Q80XX9	Q80xx9 rattus norv
2	87	14.3	333	4 Q9BZG3	Q9bzb3 homo sapien
3	87	14.3	426	4 Q9BZG2	Q9bzb2 homo sapien
4	83.5	13.7	610	10 Q943G8	Q943g8 oryza sativ
5	79.5	13.1	377	16 Q82N80	Q82n80 streptomyce
6	79	13.0	341	6 Q9N0B3	Q9n0b3 macaca fasc
7	78.5	12.9	332	10 Q42839	Q42839 hordeum vul
8	78.5	12.9	387	11 Q8VD70	Q8vd70 mus musculus
9	77.5	12.7	219	11 Q8BM15	Q8bmi5 mus musculus
10	77.5	12.7	1208	11 Q80YA8	Q80ya8 mus musculus
11	76.5	12.6	245	16 Q825R3	Q825r3 salmonella
12	76.5	12.6	732	16 Q81ZX4	Q81zx4 streptomyce
13	75.5	12.4	222	12 Q9QEE6	Q9qee6 indian citr
14	75.5	12.4	436	16 Q7U2G8	Q7u2g8 mycobacteri
15	75.5	12.4	449	16 Q53668	Q53668 mycobacteri
16	75.5	12.4	635	5 Q182B8	Q18288 caenorhabdi

17	75	12.3	370	4 Q96KN9	Q96kn9 homo sapien
18	75	12.3	411	16 Q8CXG1	Q8cxg1 oceanobacil
19	74.5	12.3	202	12 Q80MP4	Q80mp4 indian citr
20	74.5	12.3	330	7 Q860W5	Q860w5 mus musculu
21	74.5	12.3	519	16 Q9A9X4	Q9a9x4 caulobacter
22	74	12.2	768	5 P90890	P90890 caenorhabdi
23	73.5	12.1	409	16 Q82FA3	Q82fa3 streptomyce
24	73.5	12.1	730	4 Q9P2P7	Q9p2p7 homo sapien
25	73	12.0	227	10 Q04393	Q04393 hordeum vul
26	73	12.0	243	16 Q8PQD6	Q8pqd6 xanthomonas
27	73	12.0	370	4 Q8N2R7	Q8n2r7 homo sapien
28	73	12.0	768	13 Q98TH8	Q98th8 cyprinus ca
29	72.5	11.9	206	4 Q96QA0	Q96qa0 homo sapien
30	72.5	11.9	242	16 Q8NNC0	Q8nnc0 corynebacte
31	72.5	11.9	329	4 Q9NQD2	Q9nqd2 homo sapien
32	72.5	11.9	346	16 Q9RSC0	Q9rsc0 deinococcus
33	72.5	11.9	365	4 Q9Y288	Q9y288 homo sapien
34	72.5	11.9	370	4 Q9BZW8	Q9bzw8 homo sapien
35	72.5	11.9	445	2 Q7WX79	Q7wx79 alcaligenes
36	72	11.8	368	13 Q9IAR7	Q9iar7 gallus gall
37	72	11.8	721	5 Q8I8V6	Q8i8v6 giardia lam
38	71.5	11.8	210	4 Q95054	Q95054 homo sapien
39	71.5	11.8	379	10 Q8W393	Q8w393 oryza sativ
40	71.5	11.8	2873	12 Q93072	Q93072 hepatitis g
41	71	11.7	116	12 Q90631	Q90631 baboon herp
42	71	11.7	175	16 Q9S255	Q9s255 streptomyce
43	71	11.7	308	16 Q7WR57	Q7wr57 bordetella
44	71	11.7	308	16 Q7W290	Q7w290 bordetella
45	71	11.7	308	16 Q7VT68	Q7vt68 bordetella

ALIGNMENTS

RESULT 1  
Q80XX9  
ID Q80XX9 PRELIMINARY; PRT; 129 AA.  
AC Q80XX9;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Type 1 transmembrane protein FN14.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mueller A.M., Giegerich G.;  
RT "FN14, TNFRSF12a.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY255102; AAP06753.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
KW Transmembrane.  
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match	74.5%;	Score 453;	DB 11;	Length 129;
Best Local Similarity	76.1%;	Pred. No. 1.9e-39;		
Matches	86;	Conservative	5;	Mismatches 22; Indels 0; Gaps 0;
Qy	1	MARGSLRRLRLLLVLGLMLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCARPH	60	
Db	1	MAGWPRLPQLLVGLVGLVIRATAGEQAPGNAPCSSGSSWSADLDKCMDCASCARPH	60	
Qy	61	SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLVWRRRCRRSSPPP	113	
Db	61	SDFCLGCAAAAPPAPFRLWLPILGGALSLALVLSGLVWRRRCRRREKFTTP	113	

RESULT 2  
Q9BZG3  
ID Q9BZG3 PRELIMINARY; PRT; 333 AA.  
AC Q9BZG3;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Acid phosphatase variant 3.  
GN ACPT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21309073; PubMed=11414767;  
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;  
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that  
RT is highly expressed in the testis.";  
RL Genomics 74:385-395(2001).  
DR EMBL; AF321918; AAK09396.1; -.  
DR HSSP; P15309; 2HPA.  
DR GO; GO:0003993; F:acid phosphatase activity; IEA.  
DR InterPro; IPR000560; HisAc\_phosphatase.  
DR Pfam; PF00328; acid\_phosphat; 1.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;  
  
Query Match 14.3%; Score 87; DB 4; Length 333;  
Best Local Similarity 35.3%; Pred. No. 0.49;  
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;  
  
QY 31 PG-TAPCSRGSWSADLKCWCDCASCRRPHSDFCLGC--AAAPPAPFRLLPILGGALS 87  
DB 258 PGCPAPCPLGRFYQL-----TAPARPPAHGVSGHGPYEAIPAP---VVPELLAGAVA 307  
[1]  
  
QY 88 LTFVLGLLSGFLVWR-RRRERSSP 111  
DB 308 VLVALSLGLGLLAWRPGCLRALGGP 332  
[1]  
  
RESULT 3  
QYBZG2 ID Q9BZG2 PRELIMINARY; PRT; 426 AA.  
AC Q9BZG2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Acid phosphatase.  
GN ACPT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21309073; PubMed=11414767;  
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;  
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that  
RT is highly expressed in the testis.";  
RL Genomics 74:385-395(2001).  
DR EMBL; AF321918; AAK09393.1; -.  
DR HSSP; P15309; 2HPA.  
DR Genew; HGNC:14376; ACPT.  
DR GO; GO:0003993; F:acid phosphatase activity; IEA.  
DR InterPro; IPR000560; HisAc\_phosphatase.  
DR Pfam; PF00328; acid\_phosphat; 1.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
SQ SEQUENCE 426 AA; 45089 MW; BE930398041DB061 CRC64;  
  
Query Match 14.3%; Score 87; DB 4; Length 426;  
Best Local Similarity 35.3%; Pred. No. 0.62;  
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;  
  
QY 31 PG-TAPCSRGSWSADLKCWCDCASCRRPHSDFCLGC--AAAPPAPFRLLPILGGALS 87

DB 351 PGCPAPCPLGRFYQL-----TAPARPPAHGVSGHGPYEAIPAP---VVPELLAGAVA 400  
QY 88 LTFVLGLLSGFLVWR-RRRERSSP 111  
DB 401 VLVALSLGLGLLAWRPGCLRALGGP 425  
[1]  
  
RESULT 4  
QYBZG2 ID Q943G8 PRELIMINARY; PRT; 610 AA.  
AC Q943G8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative receptor protein kinase.  
GN P0046E05.12.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
RT clone:P0046E05.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AP003237; BAB67905.1; -.  
DR Gramene; Q943G8; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;  
KW Transferase.  
SQ SEQUENCE 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;  
  
Query Match 13.7%; Score 83.5; DB 10; Length 610;  
Best Local Similarity 24.6%; Pred. No. 2;  
Matches 34; Conservative 12; Mismatches 35; Indels 57; Gaps 4;  
  
QY 30 APGTAPCSRGSWSADLKCDCMD-----CASCRRPHSDF 63  
DB 84 SPGDSSYTGSGSSTSATVTASTADPNAGDAVPTSAGDAIPSSACRKPAAARCPNRPATD- 142  
QY 64 CLGCAAAAPPAPERLLWP-----ILGGALSLTFVLGLLSG- 97  
DB 143 --NVPASPPPPRISLSPPPPSTPTQTQSGASSGSKSSNNGTVVAVGVAAVVVLGLAAGL 200  
[1]  
  
QY 98 --FLVWRRRCRRERSSPPP 113  
DB 201 IYFFVSKRRRRRRQHPPPP 218  
[1]  
  
RESULT 5  
QYBZG2 ID Q82N80 PRELIMINARY; PRT; 377 AA.  
AC Q82N80;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.



GN SAV1423.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis: deducing the ability of producing secondary  
RT metabolites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
RT microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:526-531(2003).  
DR EMBL; AP005026; HAC69133.1; -.  
DR InterPro; IPR007016; Wzy\_C.  
DR Pfam; PF04932; Wzy\_C; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 377 AA; 36860 MW; 7964E23DFE6F29AA CRC64;

Query Match 13.1%; Score 79.5; DB 16; Length 377;  
Best Local Similarity 34.1%; Pred. No. 3.3;  
Matches 29; Conservative 10; Mismatches 33; Indels 13; Gaps 3;

QY 15 LGLVLAAPHGCTAGLQ--GSSPLGPAGATAALLTLCAGAACCA-----WAARPSA 157  
Db 110 LGLVLAAPHGCTAGLQ--GSSPLGPAGATAALLTLCAGAACCA-----WAARPSA 157  
QY 75 FRLWLPILGGALSLT-FVLGLLSGF 98  
Db 158 SRLALRLAAAITVTAALGSLTGF 182

RESULT 6  
Q9N0B3  
ID Q9N0B3 PRELIMINARY; PRT; 341 AA.  
AC Q9N0B3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Unnamed protein product (Gap junction protein) (Connexin).  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED  
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH  
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY  
CC SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.  
DR EMBL; AB046017; BAB01599.1; -.

DR GO; GO:0005922; C:connexon complex; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0015285; F:connexon channel activity; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000500; Connexin.  
DR Pfam; PF00029; connexin; 1.  
DR PRINTS; PR00206; CONNEXIN.  
DR SMART; SM00037; CNX; 1.  
DR PROSITE; PS00407; CONNEXINS\_1; 1.  
DR PROSITE; PS00408; CONNEXINS\_2; 1.  
KW Gap junction; Transmembrane.

SQ SEQUENCE 341 AA; 36784 MW; 4A7IDEA938F0FA0C CRC64;  
Query Match 13.0%; Score 79; DB 6; Length 341;  
Best Local Similarity 27.9%; Pred. No. 3.4;  
Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;

QY 9 LLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPHSDFCLGCA 68  
Db 119 LLRTLLEAAFGALNYLLFGFLAPNKPCT-----RPPCTGVVDCY 158  
QY 69 AAPPAPERLLWPILGGALSLTFVLGLLSGFLVMRRRERSRSP 112  
Db 159 VSRPTEKSLMLFLWAVSALSFLGLADLVCSLRLMRRRPGPP 202

RESULT 7  
Q42839  
ID Q42839 PRELIMINARY; PRT; 332 AA.  
AC Q42839;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Chitinase (EC 3.2.1.14).  
GN CHI33.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Seed;  
RX MEDLINE=95078949; PubMed=7987416;  
RA Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,  
RA Mundy J.;  
RT "Identification of an enhancer/silencer sequence directing the  
RT aleurone-specific expression of a barley chitinase gene.";  
RL Plant J. 6:579-589(1994).  
DR EMBL; L34211; AAA56787.1; -.  
DR PIR; T04484; T04484.  
DR HSSP; P23951; 2BAA.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0008843; F:endochitinase activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR GO; GO:0016998; P:cell wall catabolism; IEA.  
DR GO; GO:0006032; P:chitin catabolism; IEA.  
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.  
DR InterPro; IPR01002; Chitin binding 1.  
DR InterPro; IPR00726; Glyco\_hydro\_19.  
DR Pfam; PF00187; Chitin bind 1; 1.  
DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
DR PRINTS; PR00451; CHITINBINDG.  
DR ProDom; PD000609; Chitin binding 1; 1.  
DR ProDom; PD35490; Glyco\_hydro\_19; 1.  
DR SMART; SM00270; ChtBD1; 1.  
DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
DR PROSITE; PS00026; CHITIN\_BINDING; 1.  
KW Chitin-binding; Glycosidase; Hydrolase.  
SQ SEQUENCE 332 AA; 35369 MW; 1B38554F49AC9E0F CRC64;

Query Match 12.9%; Score 78.5; DB 10; Length 332;  
Best Local Similarity 32.0%; Pred. No. 3.7;  
Matches 33; Conservative 9; Mismatches 38; Indels 23; Gaps 7;  
QY 13 LVGLWLALLRSV-----AGEQAPG-TAP-----CSRSSWSADLDKCMDCASCRRPHSDF 63  
Db 13 IVLSAALAMAMVVRQQCGSQAGGATCPNCLCCSRFGYCGSTSDYC--GAGCQSQ----- 65  
QY 64 CLGCAAAPAPAPERLLWPILGGALSFLTFLGLLSGFLVWR-RCR 105  
Db 66 CSGCGTPPGPSP-----GGGVSSIISRLDFEQFLHRDRCQ 102

RESULT 8  
Q8VD70 PRELIMINARY; PRT; 387 AA.  
AC Q8VD70;  
DT 01-MAR-2002 (TReMBLrel. 20, Created)  
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 12.  
GN TNFRSF25 OR TNFRSF12.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary gland;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017526; AAH17526.1; -.  
DR MGD; MGI:1934667; Tnfrsf25.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Receptor.  
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match 12.9%; Score 78.5; DB 11; Length 387;  
Best Local Similarity 18.9%; Pred. No. 4.3;  
Matches 35; Conservative 21; Mismatches 44; Indels 85; Gaps 7;  
QY 4 GSLRRLRLLLVGLWLALLRSVAGE-----PAPFLLWPILGGALSFLTFLG--LLSGFLV 30  
Db 18 GSTARVLQPLFLPLLLLLLLLLGGQGGMSGRCDCASESQKRYGPFCCRCGPKGHYMK 77  
QY 31 PGTAPC-----SRGSSWSADLDKCMDC-----ASCRARP-----HS 61  
Db 78 PCAEPCGNSTCLPCPSDTFLTRDNHFKTDCTRCQVDEEALQVLENCSAKSDTHGCGQS 137  
QY 62 DFCLGCAAP-----PAPFLLWPILGGALSFLTFLG--LLSGFLV 100  
Db 138 GWCVDCSTEPCKGKSSPFCVPCGATTVPHEAPTPLFW--VQVLLGVAFLLFGAILICAYCR 195  
QY 101 WRCR 105  
Db 196 WQPC 200

RESULT 9  
Q8BMI5 PRELIMINARY; PRT; 219 AA.  
ID Q8BMI5

AC Q8BMI5;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Weakly similar to neurogenic locus notch 3 protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Forelimb;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; AK031068; BAC27237.1; -.  
DR PIR; PT0633; PT0633.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF00008; EGF; 2.  
DR SMART; SM00181; EGF; 3.  
DR SMART; SM00179; EGF\_CA; 2.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 4.  
DR PROSITE; PS01186; EGF\_2; 2.  
FT NON\_TER 1  
SQ SEQUENCE 219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;  
Query Match 12.7%; Score 77.5; DB 11; Length 219;  
Best Local Similarity 30.0%; Pred. No. 3.2;  
Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

QY 19 LALLRSVAGEQAPGTAPCSRGSW--SADLDKCMDCASCRRPHSDFCLGCAAP-PAPF 75  
Db 99 LAGLRCSQSLDKPCEASPCLINGGTCRVASGIFEC---TCSAGFSQGFCVVKTLPLPF 154  
QY 76 RLLWPILGGALS--LTFVLGLLSGFLVWRRCRRSSPPP 113  
Db 155 PLLEVAVPACACLLLLLLLGLLGGILAKRRQSEGTYS 194

RESULT 10  
Q80YA8 PRELIMINARY; PRT; 1208 AA.  
ID Q80YA8  
AC Q80YA8;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE 5930402A21 protein (Fragment).  
GN 5930402A21.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043114; AAH43114.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00008; EGF; 13.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00181; EGF; 15.
DR SMART; SM00179; EGF_CA; 13.
DR SMART; SM00282; LamG; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 8.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS01187; EGF_CA; 5.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
FT NON_TER 1
SQ SEQUENCE 1208 AA; 126978 MW; FDFE2DF2F0B2F198 CRC64;

Query Match 12.7%; Score 77.5; DB 11; Length 1208;
Best Local Similarity 30.0%; Pred. No. 16;
Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

QY 19 LALLRSVAGEQAPGTAPCSRGSW--SADLDKCMDCASCRRPHSFCLGCAAP-PAPE 75
||| : : : : : : : : : : : : : : : : : : : : : :
Db 1088 LAGLRCSLDKPCASPCLINGGTCRVASGIFEC---TCSAGFSGQFCEVVKTLPLPF 1143
||| : : : : : : : : : : : : : : : : : : : : : :

QY 76 RLLWPILGGALS--LTFVLGLLSGFLVWRRCRRSSPPP 113
||| : : : : : : : : : : : : : : : : : : : : : :
Db 1144 PLLEVAVPAACACLLLLLLLGLLGGILAAKRRQSEGTYSP 1183

RESULT 11
QZ5R3 PRELIMINARY; PRT; 245 AA.
AC QZ5R3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Flagellar biosynthetic protein Flp.
GN STY2187 OR FLIP OR T0898.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
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RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627272; CAD05727.1; -.
DR EMBL; AE016837; AAC68576.1; -.
DR GO; GO:0019861; C:flagellum; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR005837; Flp.
DR InterPro; IPR005838; TypeIII_P.
DR Pfam; PF00813; Flp; 1.
DR PRINTS; PR01302; TYPE3IMPPROT.
DR ProDom; PD002586; TypeIII_P; 1.
DR TIGREAFMS; TIGR01103; Flp; 1.
DR PROSITE; PS01060; FLIP_1; 1.
DR PROSITE; PS01061; FLIP_2; 1.
KW Flagellum; Complete proteome.
SQ SEQUENCE 245 AA; 26755 MW; C9B99331F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 16; Length 245;
Best Local Similarity 30.8%; Pred. No. 4.5;
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLRLVLGLWLALLRSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRRP--- 59
: ||| : : : : : : : : : : : : : : : : : : : : : :
Db 1 MRRLLFLSLAGLW--LFSPAAAALPGLISQPLAGGQSWLSVQTLVFTSLTFLPAIL 58

QY 60 --HSDF-----CLGCAAAPAPFRLLWPILGGALSITFVL 92
: : : : : : : : : : : : : : : : : : : : : :
Db 59 LMWTSFTRIIIVFGLLRNALGTFSPAPNQV-----LLGLALFTFFI 100

RESULT 12
QZ1ZX4 PRELIMINARY; PRT; 732 AA.
AC QZ1ZX4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PKN16 OR SAV4717.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
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OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021929; CAA17338.1; ALT_INIT.
DQ EMBL; AE006934; AAK44478.1; -.
DR PIR; B70939; B70939.
DR TIGR; MT0260; -.
DR Tuberculist; RV0246; -.
KW Complete proteome.
SQ SEQUENCE 449 AA; 46926 MW; FCE6EF930F03DIE6 CRC64;
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QY	1	MARGSLRRLRLRLVLGLWLALLRSVAGEQA--PGTAPCSRGS--WSADLDKCMDCASCR	56
Db	155	MPSGTARARILLTEVGVGAAALTAVVAATLSFVPDQHPLSRNHLLWTAAVAMAISAAICR	214
QY	57	ARPHSDFCLGCAAAPAPFRLLW-----PILGG-----	84
Db	215	ALPHR--IVPRVHAAPGLHKLIVVGWTAIRTNWYRRYLLVQVLFSGSVLGSFHSIRVA	272
QY	85	-----ALSLTFVLGLLSGFLVWRRCR	105
Db	273	AVPGDQDPDEVVAVLVFCVGLLGGIALWNRVR	304

Search completed: March 1, 2004, 16:43:54  
Job time : 42 secs

Query Match 12.4%; Score 75.5; DB 16; Length 449;  
Best Local Similarity 23.0%; Pred. No. 10;  
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2004, 10:32:18 ; Search time 40 Seconds  
(without alignments)  
452.371 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLRLLLVLGLWLA.....LSGFLVWRRCRRRSSPPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	99.8	114	AAW73409	Human secreted pro
2	571	93.9	129	AAW88506	Human liver clone
3	571	93.9	129	AAW57940	Human transmembran
4	571	93.9	129	AAU03498	Human TWEAK recept
5	571	93.9	129	ABP61512	Human NF-kB activa
6	571	93.9	129	AAU79827	Human type 1 trans
7	571	93.9	129	ABU56716	Lung cancer-associ
8	450	74.0	129	AAU79828	Mouse type 1 trans
9	433	71.2	309	AAU03500	Human TWEAK recept

10	274.5	45.1	112	21	AAW91463	Human secreted pro
11	274.5	45.1	155	21	AAW91604	Human secreted pro
12	274.5	45.1	156	21	AAW91552	Human secreted pro
13	94.5	15.5	185	23	AAE22269	Human BAFF recepto
14	92.5	15.2	185	23	AAE22266	Human BAFF recepto
15	92.5	15.2	185	23	AAE22267	Human BAFF recepto
16	91.5	15.0	185	23	AAE22270	Human BAFF recepto
17	91.5	15.0	185	23	AAE22271	Human BAFF recepto
18	89.5	14.7	185	23	AAE22268	Human BAFF recepto
19	88.5	14.6	185	23	AAE22242	Human mature JST57
20	88.5	14.6	1388	23	ABP70117	Human NOV31a. Hom
21	88.5	14.6	1388	23	ABP70118	Human NOV31b. Hom
22	87	14.3	184	23	ABB81483	Human Ztnfr12 prot
23	87	14.3	184	24	AAE35227	Human Ztnfr12 rece
24	87	14.3	184	24	ABP97721	Amino acid sequenc
25	87	14.3	266	23	AAE22243	Human JST576 (BAFF
26	87	14.3	333	23	ABG32546	Human testicular a
27	87	14.3	375	23	ABG32542	Human testicular a
28	87	14.3	426	22	ABG23348	Novel human diagno
29	87	14.3	426	23	ABG32541	Human testicular a
30	87	14.3	426	23	AAU75788	Human protein phos
31	87	14.3	426	23	AAU09880	Novel human secret
32	80.5	13.2	426	21	AAU01337	TNF receptor apopt
33	80.5	13.2	508	16	AAU80631	2B10 AMH-receptor.
34	79	13.0	224	22	AAU95174	Human protein sequ
35	79	13.0	224	24	ABR01798	Human cancer-relat
36	77	12.7	152	22	ABG26293	Novel human diagno
37	77	12.7	448	21	AAU56750	Smooth muscle prol
38	77	12.7	448	21	AAU54990	Full length mouse
39	76.5	12.6	250	21	AAU58207	Canine mature Flt-
40	76.5	12.6	276	21	AAU58208	Canine Flt-3 ligan
41	76	12.5	141	22	AAW79666	Human protein SEQ
42	75	12.3	356	23	ABJ10913	Human secreted pro
43	75	12.3	356	23	ABP60987	Novel human protei
44	75	12.3	370	23	ABP60986	Novel human protei
45	74	12.2	234	22	AAU24485	Human EST encoded

ALIGNMENTS

RESULT 1

AAW73409

ID AAW73409 standard; Protein; 114 AA.

XX

AC AAW73409;

XX

DT 19-FEB-1999 (first entry)

XX Human secreted protein encoded by Gene No. 13.

DE

XX Secreted protein; human; protein therapy; gene therapy; blood disorder;

KW pathological condition; diagnosis; cancer; neurological disorder;

KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;

KW immune system disorder; Alzheimer's disease; cognitive disorder;

KW schizophrenia; prostate disease; autoimmune disorder; AIDS.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Misc-difference 114

FT /note= "unspecified amino acid"

XX

PN WO9854206-A1.

XX

PD 03-DEC-1998.

XX

PF 28-MAY-1998; 98WO-US10868.

XX

PR 29-AUG-1997; 97US-0056296.

PR 30-MAY-1997; 97US-0044039.

PR 30-MAY-1997; 97US-0048093.

PR 30-MAY-1997; 97US-0048101.

PR 30-MAY-1997; 97US-0048190.  
PR 30-MAY-1997; 97US-0048356.  
PR 30-MAY-1997; 97US-0050935.  
PR 29-AUG-1997; 97US-0056250.  
PR 29-AUG-1997; 97US-0056293.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA Carter KC, Dillon PJ, Endress GA, Feng P, Ni J;  
PI Rosen CA, Ruben SM, Yu G;  
PI  
XX  
DR WPI; 1999-070209/06.  
DR N-PSDB; AAV08823.  
XX  
PT New isolated human genes - useful for diagnosis and treatment of,  
PT e.g. cancers, neurological disorders, immune diseases, developmental  
PT disorders or blood disorders  
XX  
PS Claim 11; Page 153; 188pp; English.  
XX  
CC This sequence is encoded by a cDNA of the invention, designated  
CC Gene No. 13. This sequence represents a human secreted protein, and is  
CC expressed in keratinocytes and to a lesser extent in endothelial  
CC cells and placenta.  
CC The DNA sequences of the invention and their corresponding secreted  
CC polypeptides are useful for preventing, treating or ameliorating medical  
CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
CC can be diagnosed by determining the amount of the new polypeptides in a  
CC sample or by determining the presence of mutations in the DNA sequences.  
CC Specific uses are described for each of the DNA sequences and the encoded  
CC proteins, based on which tissues they are most highly expressed in, and  
CC include developing products for the diagnosis or treatment of cancer,  
CC tumours, neurological disorders, developmental abnormalities and foetal  
CC deficiencies, blood disorders, leukaemias, diseases of the immune system  
CC (including allergies or asthma), hepatic disease, Alzheimer's and  
CC cognitive disorders, schizophrenia, prostate diseases, autoimmune  
CC disorders and AIDS. The polypeptides are also useful for identifying  
CC their binding partners.  
XX  
SQ Sequence 114 AA;  
  
Query Match 99.8%; Score 607; DB 20; Length 114;  
Best Local Similarity 100.0%; Pred. No. 6.5e-56;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRPH 60  
Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRPH 60  
  
QY 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
  
RESULT 2  
AAW88506  
ID AAW88506 standard; Protein; 129 AA.  
XX  
AC AAW88506;  
XX  
DT 30-MAR-1999 (first entry)  
XX  
DE Human liver clone HP10432-encoded membrane protein.  
XX  
KW Transmembrane protein; HP10432; human; liver.  
XX  
OS Homo sapiens.  
XX  
PN WO9855508-A2.  
XX  
PD 10-DEC-1998.  
XX  
PF 03-JUN-1998; 98WO-JP02445.

XX 03-JUN-1997; 97JP-0144948.  
PR (PROT-) PROTEGENE INC.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
XX  
PI Kato S, Sekine S, Yamaguchi T;  
XX  
DR WPI; 1999-045730/04.  
DR N-PSDB; AAV84374.  
XX  
PT New human proteins containing transmembrane domains and their  
PT encoding sequences - useful in the preparation of antibodies and  
PT large-scale protein production, gene diagnosis, and gene therapy  
XX  
PS Claim 1; Page 152-153; 178pp; English.  
XX  
CC This is the amino acid sequence of a transmembrane protein encoded  
CC by human liver cDNA clone HP10432 (see AAV84374). The encoded protein  
CC has a signal-like N-terminal region and one internal transmembrane  
CC domain. The invention provides nucleotide sequences (see AAV84359-76)  
CC coding for 18 transmembrane proteins (see AAW88491-508), vectors  
CC containing such polynucleotides, and eukaryotic cells containing the  
CC vectors. The proteins can be used as antigens or as compositions  
CC in the preparation of antibodies against the proteins. The  
CC polynucleotides can be used as probes for gene diagnosis, and as  
CC gene sources for gene therapy and large-scale production of proteins  
CC encoded by the cDNA. The host cells are used for the detection of  
CC ligands corresponding to the expressed proteins, and the screening  
CC of low mol.wt. medicines.  
XX  
SQ Sequence 129 AA;  
  
Query Match 93.9%; Score 571; DB 20; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRPH 60  
Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRPH 60  
  
QY 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGLLSGFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGLLSGFLVWRRRRREKFTTP 113  
  
RESULT 3  
AAW57940  
ID AAY57940 standard; Protein; 129 AA.  
XX  
AC AAY57940;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Human transmembrane protein HTMPN-64.  
XX  
KW Human; transmembrane protein; HTMPN; diagnosis; immunospecific;  
KW antiproliferative; neuroprotective; immune disorder;  
KW reproductive disorder; smooth muscle disorder; neurological disorder;  
KW gastrointestinal disorder; developmental disorder;  
KW cell proliferative disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO9961471-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11904.  
XX  
PD 29-MAY-1998; 98US-0087260.  
PR 02-JUL-1998; 98US-0091674.  
PR 02-OCT-1998; 98US-0102954.

PR 24-NOV-1998; 98US-0109869.  
XX (INCY-) INCYTE PHARM INC.  
XX  
PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;  
PI Au-Young J;  
XX  
DR WPI; 2000-072605/06.  
DR N-PSDB; AAZ56761.  
XX  
PT Proteins, polynucleotides, vectors, host cells and antibodies used to  
PT diagnose, treat or prevent immune, reproductive, smooth muscle,  
PT neurological, gastrointestinal, developmental and cell proliferative  
PT disorders -  
XX  
PS Claim 1; Page 163; 229pp; English.  
XX  
CC AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human  
CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively.  
CC The transmembrane protein have immunospecific, antiproliferative and  
CC neuroprotective activities. The human transmembrane proteins,  
CC polynucleotides encoding them and other compositions and methods from  
CC the present invention, can be used for the diagnosis, treatment or  
CC prevention of immune, reproductive, smooth muscle, neurological,  
CC gastrointestinal, developmental and cell proliferative disorders. The  
CC HTMPN's can be used to treat or prevent disorders associated with a  
CC decreased expression or activity of HTMPN.  
XX  
SQ Sequence 129 AA;  
  
Query Match 93.9%; Score 571; DB 21; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MARGSLRRLRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
  
QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRRRSSPPPP 113  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRRRRRREKFTTP 113  
  
RESULT 4  
AAU03498  
ID AAU03498 standard; Protein; 129 AA.  
XX  
AC AAU03498;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE Human TWEAK receptor (TWEAKR) polypeptide.  
XX  
KW TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;  
KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;  
KW corneal graft neovascularisation; psoriasis; metastatic condition;  
KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
KW peripheral atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..27  
FT /note= "Signal peptide"  
FT Protein 28..129  
FT /note= "Mature human TWEAKR protein"  
FT Domain 1..78

FT Domain /note= "Extracellular domain"  
FT 79..101  
FT /note= "Transmembrane domain"  
FT 102..129  
FT /note= "Intracellular domain"  
XX  
PN WO200145730-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 19-DEC-2000; 2000WO-US34755.  
XX  
PR 20-DEC-1999; 99US-0172878.  
PR 10-MAY-2000; 2000US-0203347.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Wiley SR;  
XX  
DR WPI; 2001-417975/44.  
DR N-PSDB; AAS03963.  
XX  
PT Modulating angiogenesis in a mammal for treating diseases mediated by  
PT angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or  
PT peripheral tissue, by administering antagonist or agonist of TWEAK  
PT receptor -  
XX  
PS Example 1; Fig 1; 46pp; English.  
XX  
CC The sequence represents the human TWEAK receptor (TWEAKR) protein. The  
CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and  
CC induces angiogenesis. TWEAKR may therefore be used to screen for and  
CC develop TWEAKR agonists and antagonists for the modulation of  
CC angiogenesis, to be used in the treatment and diagnosis of human disease.  
CC The disorders mediated by angiogenesis include ocular disorders  
CC characterised by ocular neovascularisation such as diabetic retinopathy,  
CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,  
CC retrolental fibroplasia, rubeosis, uveitis, macular degeneration and  
CC corneal graft neovascularisation, and inflammatory diseases such as  
CC arthritis, rheumatism and psoriasis. Other treatable diseases include  
CC malignant and metastatic conditions such as sarcomas and carcinomas,  
CC benign tumours and preneoplastic conditions, myocardial angiogenesis,  
CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic  
CC plaque neovascularisation, telangiectasia, wound granulation, coronary  
CC atherosclerosis, peripheral atherosclerosis and ischaemia.  
XX  
SQ Sequence 129 AA;  
  
Query Match 93.9%; Score 571; DB 22; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MARGSLRRLRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
  
QY 61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRRRSSPPPP 113  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 SDFCLGCAAAAPPAPFRLLWPILGGALSLTFVLGSLGFLVWRRRRRRREKFTTP 113  
  
RESULT 5  
ABP61512  
ID ABP61512 standard; Protein; 129 AA.  
XX  
AC ABP61512;  
XX  
DT 30-SEP-2002 (first entry)  
XX  
DE Human NF-kB activating protein SEQ ID NO 178.  
XX  
KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;



KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200253737-A1.  
XX  
PD 11-JUL-2002.  
XX  
PF 25-DEC-2001; 2001WO-JP11389.  
XX  
PR 28-DEC-2000; 2000JP-0402288.  
PR 26-MAR-2001; 2001JP-0088912.  
PR 24-AUG-2001; 2001JP-0254018.  
XX  
PA (ASAH ) ASahi KASEI KOGYO KK.  
XX  
PI Matsuda A, Honda G, Muramatsu S, Nagano Y;  
XX  
DR WPI; 2002-583617/62.  
DR N-PSDB; ABQ92000.  
XX  
PT NF-approximatelykB activating gene and expressed protein, applicable in  
PT diagnosis and screening inhibitors or promoters to control excessive  
PT activation or inhibition for treating e.g. inflammations, autoimmune  
PT diseases and cancer -  
XX  
PS Claim 4; Page 814-815; 841pp; Japanese.  
XX  
CC The invention relates to a purified protein (I), comprising one of 90  
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
CC the sequences but with some amino acids deleted, substituted or added and  
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
CC inhibitors or promoters to control excessive activation or inhibition  
CC and for treating e.g. inflammations, autoimmune diseases, cancers,  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders.  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 23; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLGFLVWRRRCRRSSPPP 113  
Db 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLGFLVWRRRCRRREKFTTP 113  
RESULT 6  
AAU79827  
ID AAU79827 standard; Protein; 129 AA.  
XX  
AC AAU79827;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human type 1 transmembrane protein Fn14.  
XX  
KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
KW vulnerable; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
XX  
OS Homo sapiens.

XX WO200222166-A2.  
PN  
XX  
PD 21-MAR-2002.  
XX  
PF 12-SEP-2001; 2001WO-US28451.  
XX  
PR 14-SEP-2000; 2000US-232355P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Browning J, Burkly L, Jakubowski A, Zheng T;  
XX  
DR WPI; 2002-383103/41.  
XX  
PT Methods of modulating angiogenesis and inhibiting tumour progression,  
PT using TWEAK receptor agonists -  
XX  
PS Disclosure; Fig 10A; 37pp; English.  
XX  
CC The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention.  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 23; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60  
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLGFLVWRRRCRRSSPPP 113  
Db 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLGFLVWRRRCRRREKFTTP 113  
RESULT 7  
ABU56716  
ID ABU56716 standard; Protein; 129 AA.  
XX  
AC ABU56716;  
XX  
DT 02-APR-2003 (first entry)  
XX  
DE Lung cancer-associated polypeptide #309.  
XX  
KW Lung cancer-associated polypeptide; cytostatic; emphysema;  
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
XX  
OS Unidentified.  
XX  
PN WO200286443-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 18-APR-2002; 2002WO-US12476.  
XX  
PR 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.  
PR 09-NOV-2001; 2001US-339245P.  
PR 13-NOV-2001; 2001US-350666P.  
PR 29-NOV-2001; 2001US-334370P.  
PR 12-APR-2002; 2002US-372246P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Aziz N, Murray R;  
XX  
DR WPI; 2003-093161/08.  
DR N-PSDB; ABX76445.  
XX  
PT Detecting a lung cancer-associated transcript in a cell from a patient  
PT for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased  
PT expression in lung cancer  
XX  
PS Claim 27; Page 429; 453pp; English.  
XX  
CC The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung  
CC cancer-associated polynucleotides and polypeptides are used for  
CC identifying a compound that modulates a lung cancer-associated  
CC polypeptide, for inhibiting proliferation of a lung cancer-associated  
CC cell to treat lung cancer in a patient and for treating a mammal having  
CC lung cancer by administering a modulatory compound identified. The  
CC methods are useful for treating lung cancer, such as small cell lung  
CC cancer, non-small cell lung cancer or other benign or precancerous  
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive  
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial  
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides  
CC and polypeptides are useful for diagnostic purposes and as targets for  
CC screening for therapeutic compounds that modulate lung cancer, such as  
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated  
CC polypeptides of the invention.  
XX  
SQ Sequence 129 AA;  
Query Match 93.9%; Score 571; DB 24; Length 129;  
Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRARPH 60  
Db |||||  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRARPH 60  
Db |||||  
QY 61 SDFCLGCAAAPAPFRLWLPILGALSITFVLGSLGVWRRRERSPPPP 113  
Db |||||  
QY 61 SDFCLGCAAAPAPFRLWLPILGALSITFVLGSLGVWRRRERSPPPP 113  
Db |||||  
RESULT 8  
AAU79828  
ID AAU79828 standard; Protein; 129 AA.  
XX  
AC AAU79828;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Mouse type 1 transmembrane protein Fn14.  
XX  
KW Type 1 transmembrane protein Fn14; mouse; cytostatic; cardiant;  
KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
XX

OS Mus musculus.  
XX  
PN WO200222166-A2.  
XX  
PD 21-MAR-2002.  
XX  
XX 12-SEP-2001; 2001WO-US28451.  
PF  
XX 14-SEP-2000; 2000US-232355P.  
PR  
XX (BIOJ ) BIOGEN INC.  
PA  
XX  
PI Browning J, Burkly L, Jakubowski A, Zheng T;  
XX  
DR WPI; 2002-383103/41.  
XX  
PT Methods of modulating angiogenesis and inhibiting tumour progression,  
PT using TWEAK receptor agonists  
XX  
PS Disclosure; Fig 10B; 37pp; English.  
XX  
CC The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the mouse type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention.  
XX  
SQ Sequence 129 AA;  
Query Match 74.0%; Score 450; DB 23; Length 129;  
Best Local Similarity 75.2%; Pred. No. 2.1e-39;  
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRARPH 60  
Db |||||  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRARPH 60  
Db |||||  
QY 61 SDFCLGCAAAPAPFRLWLPILGALSITFVLGSLGVWRRRERSPPPP 113  
Db |||||  
QY 61 SDFCLGCAAAPAPFRLWLPILGALSITFVLGSLGVWRRRERSPPPP 113  
Db |||||  
RESULT 9  
AAU03500  
ID AAU03500 standard; Protein; 309 AA.  
XX  
AC AAU03500;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.  
XX  
KW TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;  
KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
KW rubecosis; uveitis; macular degeneration; arthritis; rheumatism;  
KW corneal graft neovascularisation; psoriasis; metastatic condition;  
KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
KW peripheral atherosclerosis; human IgG1; TWEAKR-Fc; fusion protein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT Peptide 1..27 /note= "Signal peptide"  
FT Protein 28..309 /note= "Mature human TWEAKR-Fc fusion protein. Specifically referred to in Claim 11"  
FT Domain 28..79 /note= "From TWEAKR extracellular domain. Specifically referred to in Claims 4 and 10"  
FT Region 80..81 /note= "From a BgIII cloning site"  
FT Region 82..309 /note= "Fc portion"  
XX WO200145730-A2.  
PN 28-JUN-2001.  
XX  
PD 19-DEC-2000; 2000WO-US34755.  
XX  
PF 20-DEC-1999; 99US-0172878.  
XX 10-MAY-2000; 2000US-0203347.  
XX (IMMV ) IMMUNEX CORP.  
XX Wiley SR;  
XX WPI; 2001-417975/44.  
DR N-PSDB; AAS03965.  
XX  
XX Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK receptor -  
PS Claim 4; Page 45-46; 46pp; English.  
XX  
CC The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKR) protein extracellular domain fused to an Fc portion from human IgG1. This fusion protein, TWEAKR-Fc, is used in the preparation of TWEAKR agonists and antagonists. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.  
XX  
SQ Sequence 309 AA;  
Query Match 71.2%; Score 433; DB 22; Length 309;  
Best Local Similarity 74.1%; Pred. No. 3.2e-37;  
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;  
QY 1 MARGSLRRLRLRLVLGLWALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLRLVLGLWALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAPAPFRLLWPIGLGALSLTFVLGLLSGFLVWRRRERSRSP 112  
Db 61 SDFCLGCAAPAPFRLL-----WRSCKTHTCPP 90

AAAY91463  
ID AAAY91463 standard; Protein; 112 AA.  
XX  
AC AAAY91463;  
XX  
DT 29-JUN-2000 (first entry)  
XX  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.  
XX  
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.  
XX  
OS Homo sapiens.  
XX  
PN WO200006698-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 29-JUL-1999; 99WO-US17130.  
XX  
PR 30-JUL-1998; 98US-0094657.  
PR 05-AUG-1998; 98US-0095486.  
PR 06-AUG-1998; 98US-0095454.  
PR 06-AUG-1998; 98US-0095455.  
PR 12-AUG-1998; 98US-0096319.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
XX  
DR WPI; 2000-195282/17.  
DR N-PSDB; AAA26358.  
XX  
PT New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -  
PT  
XX  
PS Claim 11; Page 465; 634pp; English.  
XX  
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAAY91451 to AAAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal diseases, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAAY91450 are sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 112 AA;



Query Match 45.1%; Score 274.5; DB 21; Length 112;  
Best Local Similarity 96.4%; Pred. No. 4.3e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MARGSLRRLRLLLVLGLWLLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVLGLWLLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCTSC 56  
  
RESULT 11  
AAAY91604  
ID AAY91604 standard; Protein; 155 AA.  
XX  
AC AAY91604;  
XX  
DT 29-JUN-2000 (first entry)  
XX  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:277.  
XX  
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;  
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;  
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;  
KW immune disease; inflammation; blood disorder; tumour; chromosome 16.  
XX  
OS Homo sapiens.  
XX  
PN WO200006698-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 29-JUL-1999; 99WO-US17130.  
XX  
PR 30-JUL-1998; 98US-0094657.  
PR 05-AUG-1998; 98US-0095486.  
PR 06-AUG-1998; 98US-0095454.  
PR 06-AUG-1998; 98US-0095455.  
PR 12-AUG-1998; 98US-0096319.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
XX  
DR WPI; 2000-195282/17.  
XX  
PT New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders -  
XX  
PS Disclosure; Page 36-37; 634pp; English.  
XX  
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the  
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted  
CC proteins can have activities based on the tissues and cells they are  
CC expressed in. Examples of the activities are: cytostatic;  
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;  
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;  
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their  
CC corresponding secreted proteins are useful for preventing, treating or  
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also  
CC pathological conditions can be diagnosed by determining the amount of the  
CC proteins in a sample or by determining the presence of mutations in the  
CC polynucleotides. Specific uses are described for each of the  
CC polynucleotides, based on which tissues they are most highly expressed  
CC in, and include developing products for the diagnosis or treatment of  
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities  
CC and foetal deficiencies, blood disorders, diseases of the immune system,  
CC autoimmune diseases, hepatic and renal disease, inflammation,  
CC allergies, Alzheimer's and behavioural disorders, schizophrenia,  
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,  
CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,

CC cardiovascular disorders, reproductive disorders, gastrointestinal  
CC disorders, respiratory disorders and metabolic disorders. The proteins  
CC or polynucleotides can also be used as food additives or preservatives.  
CC The proteins are also useful for identifying their binding partners.  
CC AAA26337 to AAA26345 and AAY91450 are sequences used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 155 AA;  
  
Query Match 45.1%; Score 274.5; DB 21; Length 155;  
Best Local Similarity 96.4%; Pred. No. 6.1e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MARGSLRRLRLLLVLGLWLLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVLGLWLLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCTSC 56  
  
RESULT 12  
AAAY91552  
ID AAY91552 standard; Protein; 156 AA.  
XX  
AC AAY91552;  
XX  
DT 29-JUN-2000 (first entry)  
XX  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:225.  
XX  
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;  
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;  
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;  
KW immune disease; inflammation; blood disorder; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200006698-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 29-JUL-1999; 99WO-US17130.  
XX  
PR 30-JUL-1998; 98US-0094657.  
PR 05-AUG-1998; 98US-0095486.  
PR 06-AUG-1998; 98US-0095454.  
PR 06-AUG-1998; 98US-0095455.  
PR 12-AUG-1998; 98US-0096319.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
XX  
DR WPI; 2000-195282/17.  
DR N-PSDB; AAA26447.  
XX  
PT New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders -  
XX  
PS Claim 11; Page 528; 634pp; English.  
XX  
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the  
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted  
CC proteins can have activities based on the tissues and cells they are  
CC expressed in. Examples of the activities are: cytostatic;  
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;  
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;  
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their  
CC corresponding secreted proteins are useful for preventing, treating or  
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also  
CC pathological conditions can be diagnosed by determining the amount of the



CC proteins in a sample or by determining the presence of mutations in the  
CC polynucleotides. Specific uses are described for each of the  
CC polynucleotides, based on which tissues they are most highly expressed  
CC in, and include developing products for the diagnosis or treatment of  
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities  
CC and foetal deficiencies, blood disorders, diseases of the immune system,  
CC autoimmune diseases, hepatic and renal disease, inflammation,  
CC allergies, Alzheimer's and behavioural disorders, schizophrenia,  
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,  
CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,  
CC cardiovascular disorders, reproductive disorders, gastrointestinal  
CC disorders, respiratory disorders and metabolic disorders. The proteins  
CC or polynucleotides can also be used as food additives or preservatives.  
CC The proteins are also useful for identifying their binding partners.  
CC AAA26337 to AAA26345 and AAY91450 are sequences used in the  
CC exemplification of the present invention.

XX Sequence 156 AA;  
SQ Query Match 45.1%; Score 274.5; DB 21; Length 156;  
Best Local Similarity 96.4%; Pred. No. 6.2e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 13  
AAE22269  
ID AAE22269 standard; Protein; 185 AA.

XX AAE22269;

XX 25-JUL-2002 (first entry)

XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;  
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;  
KW myasthenia gravis; hypertension; organ transplantation; drug screening;  
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;  
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;  
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;  
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;  
KW mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "Wild type Val substituted with Asn"

FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"

FT WO200224909-A2.

XX 28-MAR-2002.

XX 06-SEP-2001; 2001WO-US28006.

XX 18-SEP-2000; 2000US-233152P.

XX 21-SEP-2000; 2000US-234140P.

XX 13-FEB-2001; 2001US-268499P.

XX 14-AUG-2001; 2001US-312185P.

XX (BIOJ ) BIOGEN INC.

XX Ambrose CM, Thompson JS;

XX WPI; 2002-362428/39.

XX New human BAFF receptor proteins and nucleic acids, useful for

PT treating, preventing or delaying e.g. autoimmune diseases, cancers,  
PT inherited genetic disorders involving B-cells, cardiovascular  
XX disorders, or renal disorders -  
PS Example 17; Page -; 164pp; English.  
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and  
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour  
CC Necrosis Factor (TNF) family, which is associated with the expression of  
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are  
CC useful for treating, preventing or delaying autoimmune diseases, cancer,  
CC tumorigenic conditions or inherited genetic disorders involving B-cells,  
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal  
CC disorders, inflammation, organ transplantation and HIV. Autoimmune  
CC diseases, which can be treated or prevented by BAFF-R, include systemic  
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune  
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease  
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,  
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma  
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,  
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and  
CC monoclonal gammopathy of undetermined significance. The nucleic acids,  
CC protein, protein homologues, and antibodies may further be used in  
CC screening assays, in detection assays (chromosomal mapping, tissue typing  
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic  
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides  
CC are further useful as immunogens to raise anti-BFR antibodies, or in  
CC screening drugs or compounds that modulate BAFF-R activity or expression.  
CC The present sequence is human BAFF-R protein mutant.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown  
CC in fig 2d of the specification.

XX Sequence 185 AA;

Query Match 15.5%; Score 94.5; DB 23; Length 185;  
Best Local Similarity 27.8%; Pred. No. 0.053;  
Matches 35; Conservative 13; Mismatches 39; Indels 39; Gaps 6;

QY 23 RSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SCRA-RPHSDFCLGCAAPAPERLLWP- 80  
Db 6 RSLRGRDAPAPTPCNQACFDLLVRHCVCGLLRTPRPKP---AGAASSPAPRTALQPQ 61  
QY 81 -----ILGGA---LSLTFVLGL-LSGFLVRRRCR-----E 107  
Db 62 ESVGAGAGEAALPLGLFGAPALLGLALVLALVGLSVRRRRQRLRGASSAEAPDGD 121  
QY 108 RSSPPP 113  
Db 122 KDAPEP 127

RESULT 14  
AAE22266  
ID AAE22266 standard; Protein; 185 AA.

XX AAE22266;

XX 25-JUL-2002 (first entry)

XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.

KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;  
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;  
KW myasthenia gravis; hypertension; organ transplantation; drug screening;  
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;  
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;  
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;  
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;  
KW mutant; mutein.

XX Homo sapiens.

XX

PH Key Location/Qualifiers  
FT Misc-difference 20 /note= "Wild type Val substituted with Asn"  
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"  
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"  
FT Misc-difference 27 /note= "Wild type Leu substituted with Pro"  
XX WO200224909-A2.  
PN 28-MAR-2002.  
XX 06-SEP-2001; 2001WO-US28006.  
XX 18-SEP-2000; 2000US-233152P.  
PR 21-SEP-2000; 2000US-234140P.  
PR 13-FEB-2001; 2001US-268499P.  
PR 14-AUG-2001; 2001US-312185P.  
XX (BIOJ ) BIOGEN INC.  
XX Ambrose CM, Thompson JS;  
XX WPI; 2002-362428/39.  
XX New human BAFF receptor proteins and nucleic acids, useful for  
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,  
PT inherited genetic disorders involving B-cells, cardiovascular  
PT disorders, or renal disorders -  
XX Example 17; Page -; 164pp; English.  
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and  
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour  
CC Necrosis Factor (TNF) family, which is associated with the expression of  
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are  
CC useful for treating, preventing or delaying autoimmune diseases, cancer,  
CC tumorigenic conditions or inherited genetic disorders involving B-cells,  
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal  
CC disorders, inflammation, organ transplantation and HIV. Autoimmune  
CC diseases, which can be treated or prevented by BAFF-R, include systemic  
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune  
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease  
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,  
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma  
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,  
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and  
CC monoclonal gammopathy of undetermined significance. The nucleic acids,  
CC protein, protein homologues, and antibodies may further be used in  
CC screening assays, in detection assays (chromosomal mapping, tissue typing  
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic  
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides  
CC are further useful as immunogens to raise anti-BFR antibodies, or in  
CC screening drugs or compounds that modulate BAFF-R activity or expression.  
CC The present sequence is human BAFF-R protein mutant.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown  
CC in fig 2d of the specification.  
XX Sequence 185 AA;  
SQ  
Query Match 15.2%; Score 92.5; DB 23; Length 185;  
Best Local Similarity 27.8%; Pred. No. 0.086;  
Matches 35; Conservative 13; Mismatches 39; Indels 39; Gaps 6;  
QY 23 RSVAGEQAPGTAPCRGSSWSADLKCMDASCRA-RPHSDFCLGCAAPAPFRLLP- 80  
||: ||||| ||::: : : ||: ||||| ||: ||||| ||:  
Db 6 RSLGRDAPPTPCNQTECFDPLVRHCVACGLLTPRPKP-----AGAASSPAPRTALQPQ 61  
QY 81 -----ILGGA---LSLTFVLGL-LSGFLVWRRCR-----E 107  
: ||| ||| ||| ||| ||| : ||| : ||| :

Db 62 ESVGAGAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRRRLRGASSAEAPDGD 121  
QY 108 RSSPPP 113  
: :| |  
Db 122 KDAPEP 127  
RESULT 15  
AAE222267  
ID AAE22267 standard; Protein; 185 AA.  
XX  
AC AAE22267;  
XX  
DT 25-JUL-2002 (first entry)  
XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T.  
DE  
XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;  
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;  
KW myasthenia gravis; hypertension; organ transplantation; drug screening;  
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;  
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;  
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;  
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;  
KW mutant; mutein.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 20 /note= "Wild type Val substituted with Asn"  
FT  
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"  
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"  
FT  
XX WO200224909-A2.  
XX 28-MAR-2002.  
XX 06-SEP-2001; 2001WO-US28006.  
XX 18-SEP-2000; 2000US-233152P.  
PR 21-SEP-2000; 2000US-234140P.  
PR 13-FEB-2001; 2001US-268499P.  
PR 14-AUG-2001; 2001US-312185P.  
XX (BIOJ ) BIOGEN INC.  
XX Ambrose CM, Thompson JS;  
XX WPI; 2002-362428/39.  
XX New human BAFF receptor proteins and nucleic acids, useful for  
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,  
PT inherited genetic disorders involving B-cells, cardiovascular  
PT disorders, or renal disorders -  
XX Example 17; Page -; 164pp; English.  
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and  
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour  
CC Necrosis Factor (TNF) family, which is associated with the expression of  
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are  
CC useful for treating, preventing or delaying autoimmune diseases, cancer,  
CC tumorigenic conditions or inherited genetic disorders involving B-cells,  
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal  
CC disorders, inflammation, organ transplantation and HIV. Autoimmune  
CC diseases, which can be treated or prevented by BAFF-R, include systemic  
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune  
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease  
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,  
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma  
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,  
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and  
CC monoclonal gammopathy of undetermined significance. The nucleic acids,  
CC protein, protein homologues, and antibodies may further be used in  
CC screening assays, in detection assays (chromosomal mapping, tissue typing  
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic  
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides  
CC are further useful as immunogens to raise anti-BFR antibodies, or in  
CC screening drugs or compounds that modulate BAFF-R activity or expression.  
CC The present sequence is human BAFF-R protein mutant.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown  
CC in fig 2d of the specification.  
XX Sequence 185 AA;  
SQ  
Query Match 15.2%; Score 92.5; DB 23; Length 185;  
Best Local Similarity 27.8%; Pred. No. 0.086;  
Matches 35; Conservative 13; Mismatches 39; Indels 39; Gaps 6;  
QY 23 RSVAGEQAPGTAPCRGSSWSADLKCMDASCRA-RPHSDFCLGCAAPAPFRLLP- 80  
||: ||||| ||::: : : ||: ||||| ||: ||||| ||:  
Db 6 RSLGRDAPPTPCNQTECFDPLVRHCVACGLLTPRPKP-----AGAASSPAPRTALQPQ 61  
QY 81 -----ILGGA---LSLTFVLGL-LSGFLVWRRCR-----E 107  
: ||| ||| ||| ||| ||| : ||| : ||| :



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: February 11, 2004, 10:36:33 ; Search time 21 Seconds  
(without alignments)  
522.059 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRLLRLLLVGLWLA.....LSGFLVWRRRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	12.9	332	2 T04484	probable chitinase
2	76.5	12.6	245	2 S78698	probable export pr
3	76.5	12.6	245	2 AD0753	flagellar biosynth
4	75.5	12.4	436	2 B70939	hypothetical prote
5	75.5	12.4	635	2 T20910	hypothetical prote
6	74.5	12.3	519	2 B87353	hypothetical prote
7	74	12.2	768	2 T22758	hypothetical prote
8	73.5	12.1	261	2 G69099	probable pyruvate
9	73	12.0	227	2 T04420	ribonuclease (EC 3
10	72.5	11.9	346	2 D75303	conserved hypothet
11	72	11.8	2871	2 A55624	fibrillin-1 precur
12	71	11.7	175	2 T36798	probable transcrip
13	70.5	11.6	467	2 E95850	probable amino aci
14	70	11.5	558	2 I56545	glypican precursor
15	69.5	11.4	424	2 D75330	probable beta-lact
16	69.5	11.4	587	2 C70893	hypothetical prote
17	69	11.3	324	2 JC2395	Fas antigen precur
18	68.5	11.3	431	1 B69092	conserved hypothet
19	68.5	11.3	484	2 E75138	osmoregulated prol
20	68	11.2	480	2 B61213	hypothetical prote
21	68	11.2	683	2 T00872	probable protein k
22	67.5	11.1	384	1 T46966	diheme cytochrome
23	67.5	11.1	1008	1 GNVUUK	glycoprotein precu
24	67.5	11.1	1013	2 I50615	receptor-type prot
25	67	11.0	319	2 JC4390	bone marrow stroma
26	67	11.0	332	2 AH3572	oligopeptide trans
27	67	11.0	893	2 S51603	receptor-like tyro
28	67	11.0	898	2 S47489	receptor tyrosine
29	67	11.0	981	2 S51604	receptor-like tyro

30	67	11.0	1005	2 S49015	receptor tyrosine
31	66.5	10.9	389	2 C82987	probable MFS trans
32	66	10.9	394	2 C36942	hypothetical prote
33	66	10.9	549	2 E83085	conserved hypothet
34	66	10.9	992	1 GNWVR3	structural polypro
35	66	10.9	1053	2 T07965	reverse transcript
36	66	10.9	1766	2 A42125	trophozoite cystei
37	66	10.9	2318	2 S45306	notch 3 protein -
38	65.5	10.8	214	2 T49381	hypothetical prote
39	65.5	10.8	245	2 B36869	probable export pr
40	65.5	10.8	245	2 G90964	flagellar biosynth
41	65.5	10.8	245	2 G85812	flagellar biosynth
42	65.5	10.8	506	2 F83545	hypothetical prote
43	65.5	10.8	884	2 T02731	serine/threonine-s
44	65.5	10.8	2321	2 S78549	notch3 protein - h
45	65	10.7	196	2 F82989	conserved hypothet

ALIGNMENTS

RESULT 1  
T04484  
probable chitinase (EC 3.2.1.14) - barley  
C;Species: Hordeum vulgare (barley)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
C;Accession: T04484  
R;Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.  
Plant J. 6, 579-589, 1994  
A;Title: Identification of an enhancer/silencer sequence directing the aleurone-specific  
A;Reference number: Z15373; MUID:95078949; PMID:7987416  
A;Accession: T04484  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-332 <LEA>  
A;Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961  
C;Genetics:  
A;Gene: CHI33  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;28-69/Domain: hevein chitin-binding domain homology <HCB>  
F;85-322/Domain: plant chitinase homology <PCH>

Query Match	12.9%	Score	78.5	DB	2	Length	332
Best Local Similarity	32.0%	Pred. No.	3.5				
Matches	33	Conservative	9	Mismatches	38	Indels	23
Gaps							7
QY	13	LVLGLWLALLRSV----	AGEQAPG-TAP-----	CSRGSSWSADLDKCMDCASCRRPHSDF	63		
		:	:	:	:	:	:
Db	13	IVLSAALAMAMVVR	AQQCGSQAGGATCPNCLCCSRFGYCGSTSDYC--	GACQSQ-----	65		
QY	64	CLGCAAAAPPAPFRL	LWPILGALSLTFFVLGLLSGFLVWR-R	RCR	105		
Db	66	CSGCGTTPPGPSP-----	GGGVSSIISRDLEFLHHRDRCQ	102			

RESULT 2  
S78698  
probable export protein flip precursor - Salmonella typhimurium  
C;Species: Salmonella typhimurium  
C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000  
C;Accession: S78698  
R;Ohnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 179, 6092-6099, 1997  
A;Title: The FliO, FliP, FliQ, and FliR proteins of Salmonella typhimurium: putative com  
A;Reference number: S78696; MUID:97464436; PMID:9324257  
A;Accession: S78698  
A;Molecule type: DNA  
A;Residues: 1-245 <OHN>  
A;Cross-references: EMBL:I49021; NID:gl066860; PIDN:AAB81319.1; PID:gl066863  
A;Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are  
C;Genetics:  
A;Gene: flip



C;Function:  
A;Description: may be involved in flagellar assembly; may be involved in export of flag  
C;Superfamily: flagellar biosynthetic protein flip  
C;Keywords: flagellum; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-245/Product: probable export protein flip #status predicted <MAT>  
F;45-61/Domain: transmembrane #status predicted <TM1>  
F;89-105/Domain: transmembrane #status predicted <TM2>  
F;189-205/Domain: transmembrane #status predicted <TM3>  
F;212-228/Domain: transmembrane #status predicted <TM4>  
  
Query Match 12.6%; Score 76.5; DB 2; Length 245;  
Best Local Similarity 30.8%; Pred. No. 4.3;  
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;  
  
QY 6 LRRLLRLVLGLWLALLRSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRRP--- 59  
Db 1 MRRLLFLSLAGLW--LFSPAAAALPGLISQPLAGGGQSWLSVQTLVFITSLTFLPAIL 58  
  
QY 60 --HSDF-----CLGCAAAAPPAPFRLLWPILGGALSITFVL 92  
Db 59 LMMTSFTRIIVFGLLRNALGTPSAPPNOV-----LLGLALFLTFFI 100  
  
RESULT 3  
AD0753  
flagellar biosynthetic protein Flip [imported] - Salmonella enterica ser  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AD0753  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AD0753  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-245 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD05727.1; PID:g16503220; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY2187  
C;Superfamily: flagellar biosynthetic protein flip  
  
Query Match 12.6%; Score 76.5; DB 2; Length 245;  
Best Local Similarity 30.8%; Pred. No. 4.3;  
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;  
  
QY 6 LRRLLRLVLGLWLALLRSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRRP--- 59  
Db 1 MRRLLFLSLAGLW--LFSPAAAALPGLISQPLAGGGQSWLSVQTLVFITSLTFLPAIL 58  
  
QY 60 --HSDF-----CLGCAAAAPPAPFRLLWPILGGALSITFVL 92  
Db 59 LMMTSFTRIIVFGLLRNALGTPSAPPNOV-----LLGLALFLTFFI 100  
  
RESULT 4  
B70939  
hypothetical protein Rv0246 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C;Accession: B70939  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70939  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-436 <COL>  
A;Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA17338.1; PID:el25244  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0246  
  
Query Match 12.4%; Score 75.5; DB 2; Length 436;  
Best Local Similarity 23.0%; Pred. No. 8.4;  
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;  
  
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQA--PGTAPCSRGS--WSADLDKCMDCASC 56  
Db 142 MPSTARARILLTEVGVGALTAVVAATLSFVPDQHPLSRNIHLTLWTAAVAMAISAALCR 201  
  
QY 57 ARPHSDFCLGCAAAAPPAPFRLLW-----PILGG----- 84  
Db 202 ALPHR--IVPRVHAAPGLHKLIVYVGWTAIRTNGWYRRYLLVQVLFSGSVLGSSEHSIRVA 259  
  
QY 85 -----ALSLTFVLGLLSGFLVMRRCR 105  
Db 260 AVPGDQPDDEVAVVLFVCGVLLGGIALWNRVR 291

RESULT 5  
T20910  
hypothetical protein ZK1010.9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C;Accession: T20910; T27646  
R;McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19345  
A;Accession: T20910  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-635 <WIL>  
A;Cross-references: EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9  
A;Experimental source: clone F14F7  
R;Gardner, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20398  
A;Accession: T27646  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-635 <WI2>  
A;Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9  
A;Experimental source: clone ZK1010  
C;Genetics:  
A;Gene: CESP:ZK1010.9  
A;Map position: 3  
A;Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3  
C;Superfamily: gamma-aminobutyric acid transporter  
  
Query Match 12.4%; Score 75.5; DB 2; Length 635;  
Best Local Similarity 36.6%; Pred. No. 11;  
Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;  
  
QY 31 PGTAPCSRGSWSADLDKCMDCASCRRP--HSDFCILG--CAAAPPAPFRLLWPILGGAL 86  
Db 92 PTTAYKNGGLSF---LIAYVVGILFAVPAIHMEFALGQYAAKSPPAFRMMPILEGVG 148  
  
QY 87 SLTFVLGLLSG 97  
Db 149 WMTCLVGAIG 159

RESULT 6  
B87353  
hypothetical protein CC0837 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus



A;Molecule type: DNA  
A;Residues: 1-346 <WHI>  
A;Cross-references: GB:AE002053; GB:AE000513; NID:G6459999; PIDN:AAF11754.1; PID:G646000  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR2205  
A;Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;  
Best Local Similarity 28.8%; Pred. No. 13;  
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

QY 12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC---RAPHSD----FC 64  
Db 87 LLVTCVGLGLV--TAGSASPWTV-----MWVGALVAAFGAVLATVWHLRPAAGSLFFVFA 138  
QY 65 LGCAAA--PPAPFRLLPILGALSITFVLGLLSGFLVWRRRERRSSPPP 113  
Db 139 VGTVGALPHAPPLPALAVSGGAAALSVALGALGAWHSTRARPHELAAPP 189

RESULT 11  
A55624  
fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 02-Aug-2002  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; MUID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: GB:L29454; NID:G575509; PIDN:AAA56840.1; PID:G575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin 1; EGF homology  
F;1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;  
Best Local Similarity 25.3%; Pred. No. 75;  
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36 CSRGSSWSADLDKCMD-----CASCRRPHS-----DFCLGC 67  
Db 2040 CPEGFSWSSGRRRCQDLRMSYCYAKFEGKCSPPKSRNHSKQECCKALKGEWGDPCELC 2099  
QY 68 AAAPPAPFRLLPILGGAL 86  
Db 2100 PTEPDEAFRQICPFGSGII 2118

RESULT 12  
T36798  
probable transcription regulator soxR-like - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
C;Accession: T36798  
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21614  
A;Accession: T36798  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-175 <OLI>  
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18c  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SCI30A.18c

Query Match 11.7%; Score 71; DB 2; Length 175;

Best Local Similarity 29.0%; Pred. No. 11;  
Matches 29; Conservative 12; Mismatches 33; Indels 26; Gaps 5;  
QY 2 ARGSLRRLRLLV---LGLWLALLRSVAGEQAPGTAP-----CSRGSSWSADLDKCMDCA 53  
Db 49 ARDALRRVAFVRAAQRVGIPLATIREALAEPLPEGRTPTEDDWARLSESWRSELDERIKQL 108  
QY 54 SCRAPHSDFCGLGCAAAPAPFRLLPILGGALSITFVL 92  
Db 109 N-RLRDHLTDCIGC-----GCLSETCVL 131

RESULT 13  
E95850  
probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C;Accession: E95850  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: E95850  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <KUR>  
A;Cross-references: GB:AL591985; PIDN:CAC48469.1; PID:GL5139941; GSPDB:GN00167  
A;Experimental source: strain 1021, megaplasmid pSymb  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: Smb20069  
A;Genome: plasmid  
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;  
Best Local Similarity 26.4%; Pred. No. 26;  
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLWL-----ALLRSVAGEQA-PGTAPCSRGS-----SWSADLD 47  
Db 322 LAIMVGVWASGETGAVLSSAAFEALPG-----YGNVLVTISLALFAFTTILGWAYAE 376  
QY 48 KCMDCASCRRPHSDFCGLGCAAAPAPFRLLPILWPI---LGGALSITF 90  
Db 377 KCW-----EYLIGTASA--IPFRIVTWVAVFFGATLSLDF 409

RESULT 14  
I56545  
glypican precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 31-Jan-2000  
C;Accession: I56545; JCI281; FC1132  
R;Litwack, E.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.  
J. Neurosci. 14, 3713-3724, 1994  
A;Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-an  
A;Reference number: I56545; MUID:94267529; PMID:8207484  
A;Accession: I56545  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-558 <RES>  
A;Cross-references: GB:I34067; NID:G506416; PIDN:AAA41251.1; PID:G506417  
R;Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.  
Biochem. Biophys. Res. Commun. 188, 395-401, 1992  
A;Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a

A;Reference number: JCl281; MUID:93038690; PMID:1417860  
A;Accession: JCl281  
A;Molecule type: mRNA  
A;Residues: 1-20,'T',22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>  
A;Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425  
A;Experimental source: brain  
A;Accession: PC1132  
A;Molecule type: protein  
A;Residues: 24-55;424-445 <KA2>  
C;Superfamily: glypican  
C;Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; heparan  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-530/Product: glypican #status predicted <MAT>  
F;531-558/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;55,486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
F;79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;399,512/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F;530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 11.5%; Score 70; DB 2; Length 558;  
Best Local Similarity 37.7%; Pred. No. 33;  
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLVLGLWLA--LLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCR---ARPHSDFC 64  
Db 221 RSFVQGLGVASDVVRKVA--QVPLAECRA-----VMKLIVYCAHCRGVPGARPCPDYC 272

QY 65 ----LGCAA 69  
Db 273 RNVKGCIA 281

RESULT 15  
D75330  
probable beta-lactamase - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C;Accession: D75330  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: D75330  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-424 <WHI>  
A;Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645977  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR1985  
A;Map position: 1

Query Match 11.4%; Score 69.5; DB 2; Length 424;  
Best Local Similarity 29.7%; Pred. No. 30;  
Matches 30; Conservative 11; Mismatches 35; Indels 25; Gaps 4;

QY 3 RGSRLRLRLLLVLGLWLAALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCR----- 57  
Db 2 RGTIRLTLLALLLG-----AGINACRNREAQDTAPPAQAAQSQAAAPRKAASASPAPTATE 58

QY 58 ----RPHSDFCLGCAA-----PPAPFRLWPIILGGALS 88  
Db 59 PAVSAPAADGCLPAAPAVTQAPRPPQP-----LSGRLLGL 92

Search completed: February 11, 2004, 10:39:54  
Job time : 24 secs



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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:32:48 ; Search time 13 Seconds  
(without alignments)  
412.388 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLRLLLVLGLWLA.....LSGFLVWRRRRSSPPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	93.9	129	1 FN14 HUMAN	Q9np84 homo sapien
2	445	73.2	129	1 FN14 MOUSE	Q9cr75 m tumor nec
3	87	14.3	184	1 T13C HUMAN	Q96rj3 homo sapien
4	78	12.8	448	1 FBL5 RAT	Q9wvh8 rattus norv
5	77	12.7	448	1 FBL5 MOUSE	Q9wvh9 mus musculu
6	76.5	12.6	245	1 FLIP_SALTY	P54700 salmonella
7	73.5	12.1	81	1 FORD_METH	P56815 methanobact
8	72	11.8	1278	1 NPC1 HUMAN	O15118 homo sapien
9	72	11.8	2871	1 FEN1 MOUSE	Q61554 mus musculu
10	70	11.5	443	1 FBL4 MOUSE	Q9wvj9 mus musculu
11	70	11.5	558	1 GPC1 RAT	P35053 rattus norv
12	69.5	11.4	495	1 MLP2 DROME	Q24400 drosophila
13	69	11.3	180	1 PTTG HUMAN	P53801 homo sapien
14	69	11.3	314	1 Y127 HUMAN	Q14140 homo sapien
15	69	11.3	324	1 TNR6 RAT	Q63199 rattus norv
16	68.5	11.3	205	1 GSCL HUMAN	O15499 homo sapien
17	68.5	11.3	431	1 YG84 METH	O27719 methanobact
18	67.5	11.1	368	1 GP62 HUMAN	Q9bzj7 homo sapien
19	67.5	11.1	1008	1 VGLM_UUK	P09613 ukuniemi v
20	67.5	11.1	1013	1 EPA5_CHICK	P54755 gallus gall
21	67	11.0	319	1 BST1 RAT	Q63072 rattus norv
22	67	11.0	386	1 HXAD MOUSE	Q62424 mus musculu
23	67	11.0	1005	1 EPA5 RAT	P54757 rattus norv
24	67	11.0	2871	1 FBN1_PIG	Q9tv36 sus scrofa
25	66.5	10.9	443	1 FBL4_CRIGR	O55058 cricetus
26	66	10.9	394	1 Y6B9_PSEAE	P42514 pseudomonas
27	66	10.9	992	1 POLS_RUBVM	P08563 rubella vir
28	66	10.9	1238	1 JAG2_HUMAN	Q9y219 homo sapien
29	66	10.9	2318	1 NTC3_MOUSE	Q61982 mus musculu
30	66	10.9	2319	1 NTC3 RAT	Q9r172 rattus norv
31	65.5	10.8	245	1 FLIP_ECOLI	P33133 escherichia
32	65.5	10.8	2321	1 NTC3_HUMAN	Q9um47 homo sapien
33	65	10.7	453	1 HRA3_HUMAN	P83110 homo sapien

RESULT 1				
FN14_HUMAN				
ID	FN14_HUMAN	STANDARD;	PRT;	129 AA.
AC	Q9NPB4; Q9HCS0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member Fn14 precursor			
DE	(Fibroblast growth factor-inducible immediate-early response protein			
DE	14) (FGF-inducible 14) (Tweak-receptor) (TweakR).			
GN	TNFRSF12A OR FN14.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=20216634; PubMed=10751351;			
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,			
RA	Testa J.R., Peifley K.A., Winkles J.A.;			
RT	"The Fn14 immediate-early response gene is induced during liver			
RT	regeneration and highly expressed in both human and murine			
RT	hepatocellular carcinoma."			
RL	Am. J. Pathol. 156:1253-1261(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Tanaka S., Sugimachi K.;			
RT	"Human homologue of Fn14.";			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Uterus;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	FUNCTION.			

34	65	10.7	1014	1	BPB6_MOUSE	O08644 mus musculu
35	65	10.7	1445	1	PTPG_HUMAN	P23470 homo sapien
36	64.5	10.6	123	1	VST1_HEVME	Q03499 hepatitis e
37	64.5	10.6	300	1	TR6B_HUMAN	O95407 homo sapien
38	64.5	10.6	443	1	FBL4_HUMAN	O95967 homo sapien
39	64	10.5	1210	1	EGFR_MOUSE	Q01279 mus musculu
40	64	10.5	1227	1	B3A3_MOUSE	P16283 mus musculu
41	63.5	10.4	253	1	KLK7_HUMAN	P49862 homo sapien
42	63.5	10.4	301	1	SC01_HUMAN	O75880 homo sapien
43	63.5	10.4	363	1	PSPB_CANFA	P17129 canis famil
44	63.5	10.4	430	1	PYRC_MYCTU	P71809 mycobacteri
45	63.5	10.4	476	1	HRA4_HUMAN	P83105 homo sapien

ALIGNMENTS

RX MEDLINE=21585797; PubMed=11728344;  
RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,  
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;  
RT "A novel TNF receptor family member binds TWEAK and is implicated in  
RT angiogenesis.";  
RL Immunity 15:837-846(2001).  
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in  
CC some cell types. Promotes angiogenesis and the proliferation of  
CC endothelial cells. May modulate cellular adhesion to matrix  
CC proteins.  
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
CC TRAF3.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9NP84-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9NP84-2; Sequence=VSP\_006519;  
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and  
CC kidney. Intermediate expression in lung, skeletal muscle and  
CC pancreas.  
CC -!- INDUCTION: By fibroblast growth factor 1 (FGF1) and phorbol ester.  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF191148; AAF69108.1; -;  
DR EMBL; AB035480; BAA94792.1; -;  
DR EMBL; AB035481; BAB17850.1; -;  
DR EMBL; BC002718; AAH02718.1; -;  
DR Genew; HGNC:18152; TNFRSF12A.  
DR MIM; 605914; -;  
DR GO; GO:0006928; P:cell motility; TAS.  
DR GO; GO:0007275; P:development; TAS.  
DR InterPro; IPR001368; TNFR c6.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;  
KW Alternative splicing.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 129 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER FN14.  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT TNFR-CYS (ATYPICAL).  
FT POTENTIAL.  
FT Missing (in isoform 2).  
FT /FTId=VSP\_006519.  
FT /FTId=VSP\_006519.  
SQ SEQUENCE 129 AA; 13911 MW; BF3FDFB9C1E1C448 CRC64;  
Query Match 93.9%; Score 571; DB 1; Length 129;  
Best Local Similarity 94.7%; Pred. No. 7.3e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTPCSRGSWSADLDKMDCASCRARPH 60  
Db |||||  
QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTPCSRGSWSADLDKMDCASCRARPH 60  
Db |||||  
QY 61 SDFCLGCAAPAPFRLWLPILGALSFTFVGLLSGFLVWRRRCRRRSSPPP 113  
Db |||||  
QY 61 SDFCLGCAAPAPFRLWLPILGALSFTFVGLLSGFLVWRRRCRRREKFTTP 113  
Db |||||  
RESULT 2

FN14 MOUSE  
ID FN14 MOUSE STANDARD; PRT; 129 AA.  
AC Q9CR75; Q9QZW3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
DE (Fibroblast growth factor-inducible immediate-early response protein  
DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)  
DE (Tweak-receptor) (TweakR).  
GN TNFRSF12A OR FN14 OR FGFRP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Fibroblast;  
RX MEDLINE=200297; PubMed=10551889;  
RA Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,  
RA Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA Richards C.M., Winkles J.A.;  
RT "The mitogen-inducible Fn14 gene encodes a type I transmembrane  
RT protein that modulates fibroblast adhesion and migration.";  
RL J. Biol. Chem. 274:33166-33176(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).





```
QY 108 RSSPPP 113
Db 121 KDAPEP 126

RESULT 4
FBL5_RAT
ID FBL5_RAT STANDARD; PRT; 448 AA.
AC Q9WVH8; Q9R284;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
DE protein) (EVEC).
GN FBLN5 OR DANCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99278197; PubMed=10347091;
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein
RT upregulated in embryonic and diseased adult vasculature.";
RL Circ. Res. 84:1166-1176(1999).
CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC DEVELOPMENT AND REMODELING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC -----
DR EMBL; AF112153; AAD41769.1; -
DR EMBL; AF137350; AAD25101.1; -
DR HSP; P00736; IAPQ.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
KW Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 448 FIBULIN-5.
FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 131 144 BY SIMILARITY.
FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 155 166 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 177 190 BY SIMILARITY.
FT DISULFID 192 205 BY SIMILARITY.
FT DISULFID 211 221 BY SIMILARITY.
FT DISULFID 217 230 BY SIMILARITY.
FT DISULFID 232 245 BY SIMILARITY.
FT DISULFID 251 262 BY SIMILARITY.
FT DISULFID 258 271 BY SIMILARITY.
FT DISULFID 273 286 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 299 314 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 238 238 L -> P (IN REF. 2).
SQ SEQUENCE 448 AA; 50160 MW; E6BC68F7BF14B714 CRC64;

Query Match 12.8%; Score 78; DB 1; Length 448;
Best Local Similarity 24.1%; Pred. No. 2.2;
Matches 26; Conservative 8; Mismatches 24; Indels 50; Gaps 5;

QY 6 LRRLLRLVLGLWLLRLSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRRPHSDF 63
Db 4 LKRILTVTILALWL-----PFGNAQQCTNGFDLDRQTGCGLDIDECRTIPEA-- 52
QY 64 CLG-----C-----AAAPPAP 74
Db 53 CRGDMCMVQNGGYLCIPRTNPFVVRGPNYPSTSYSGPYPAAPPVP 100

RESULT 5
FBL5_MOUSE
ID FBL5_MOUSE STANDARD; PRT; 448 AA.
AC Q9WVH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance).
GN FBLN5 OR DANCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483(1999).
CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC DEVELOPMENT AND REMODELING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC -----
DR EMBL; AF112153; AAD41769.1; -
DR EMBL; AF137350; AAD25101.1; -
DR HSP; P00736; IAPQ.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
KW Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 448 FIBULIN-5.
FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
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RL Am. J. Hum. Genet. 65:1321-1329 (1999).  
RN [8]  
RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.  
RX MEDLINE=99408226; PubMed=10480349;  
RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,  
RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,  
RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,  
RA Ohno K.;  
RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease  
RT type C.";  
RL Hum. Genet. 105:10-16 (1999).  
RN [9]  
RP VARIANTS NPC1 GLN-958 AND ALA-1007.  
RX MEDLINE=21313111; PubMed=11349231;  
RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,  
RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;  
RT "Niemann-Pick C variant detection by altered sphingolipid trafficking  
RT and correlation with mutations within a specific domain of NPC1.";  
RL Am. J. Hum. Genet. 68:1361-1372 (2001).  
RN [10]  
RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.  
RX MEDLINE=21313105; PubMed=11333381;  
RA Millat G., Marçais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,  
RA Wenger D.A., Ohno K., Vanier M.T.;  
RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels  
RT of NPC1 protein, and phenotypes emphasize the functional significance  
RT of the putative sterol-sensing domain and of the cysteine-rich  
RT luminal loop.";  
RL Am. J. Hum. Genet. 68:1373-1385 (2001).  
RN [11]  
RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.  
RX MEDLINE=21372069; PubMed=11479732;  
RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,  
RA Millat G.;  
RT "Niemann-Pick type C disease: NPC1 mutations associated with severe  
RT and mild cellular cholesterol trafficking alterations.";  
RL Hum. Genet. 109:24-32 (2001).  
CC -!- FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF  
CC CHOLESTEROL. MAY PLAY A ROLE IN VESICULAR TRAFFICKING IN GLIA, A  
CC PROCESS THAT MAY BE CRUCIAL FOR MAINTAINING THE STRUCTURAL AND  
CC FUNCTIONAL INTEGRITY OF NERVE TERMINALS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE  
CC ENDOSOMES AND LYOSOMES.  
CC -!- DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN  
CC CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYOSOMAL TARGETING  
CC ARE CRITICAL FOR MOBILIZATION OF CHOLESTEROL FROM LYOSOMES.  
CC -!- PTM: GLYCOSYLATED.  
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
CC type C1 (NPC1) [MIM:257220]; an autosomal recessive lipid storage  
CC disorder, which affects particularly the brain, liver and spleen,  
CC and which is characterized by lysosomal accumulation of low  
CC density lipoprotein derived cholesterol. Clinical features include  
CC variable hepatosplenomegaly and severe progressive neurological  
CC dysfunction such as ataxia, dystonia and dementia. The age of  
CC onset can vary from infancy to late adulthood.  
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
CC type D (NPD) [MIM:257250]; also called Niemann-Pick disease  
CC without sphingomyelinase deficiency, or Nova Scotian type. Because  
CC of evidence from biochemical changes, lack of complementation, and  
CC linkage mapping to the same chromosome site, NPD and NPC1 are  
CC considered to be allelic disorders.  
CC -!- SIMILARITY: BELONGS TO THE PATCHED FAMILY.  
CC  
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CC  
CC EMBL; AF002020; AAB63982.1; -  
CC EMBL; AF157379; AAD48006.1; -

DR EMBL; AF157365; AAD48006.1; JOINED.  
DR EMBL; AF157366; AAD48006.1; JOINED.  
DR EMBL; AF157367; AAD48006.1; JOINED.  
DR EMBL; AF157368; AAD48006.1; JOINED.  
DR EMBL; AF157369; AAD48006.1; JOINED.  
DR EMBL; AF157370; AAD48006.1; JOINED.  
DR EMBL; AF157371; AAD48006.1; JOINED.  
DR EMBL; AF157372; AAD48006.1; JOINED.  
DR EMBL; AF157373; AAD48006.1; JOINED.  
DR EMBL; AF157374; AAD48006.1; JOINED.  
DR EMBL; AF157375; AAD48006.1; JOINED.  
DR EMBL; AF157376; AAD48006.1; JOINED.  
DR EMBL; AF157377; AAD48006.1; JOINED.  
DR EMBL; AF157378; AAD48006.1; JOINED.  
DR EMBL; AF338230; AAK25791.1; -  
DR EMBL; AF123046; AAF28875.1; -  
DR EMBL; AF123045; AAF28875.1; JOINED.  
DR Genew; HGNC:7897; NPC1.  
DR MIM; 607623; -  
DR MIM; 257220; -  
DR MIM; 257250; -  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005764; C:lysosome; TAS.  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0005478; F:intracellular transporter activity; TAS.  
DR GO; GO:0015248; F:sterol transporter activity; TAS.  
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.  
DR InterPro; IPR004765; NP\_C type.  
DR InterPro; IPR003392; Patched.  
DR InterPro; IPR000731; SSD 5TM.  
DR Pfam; PF02460; Patched; 1.  
DR TIGRFAMS; TIGR00917; 2A060601; 1.  
DR PROSITE; PS50156; SSD; 1.  
KW Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;  
KW Disease mutation.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 1278 NIEMANN-PICK C1 PROTEIN.  
FT DOMAIN 249 259 POLY-PRO.  
FT DOMAIN 1275 1278 DI-LEUCINE MOTIF.  
FT TRANSMEM 270 290 POTENTIAL.  
FT TRANSMEM 351 371 POTENTIAL.  
FT TRANSMEM 622 642 POTENTIAL.  
FT TRANSMEM 655 675 POTENTIAL.  
FT TRANSMEM 678 698 POTENTIAL.  
FT TRANSMEM 760 780 POTENTIAL.  
FT TRANSMEM 833 853 POTENTIAL.  
FT TRANSMEM 1099 1119 POTENTIAL.  
FT TRANSMEM 1125 1145 POTENTIAL.  
FT TRANSMEM 1196 1216 POTENTIAL.  
FT TRANSMEM 1228 1248 POTENTIAL.  
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 11.8%; Score 72; DB 1; Length 1278;  
Best Local Similarity 31.4%; Pred. No. 21;  
Matches 27; Conservative 8; Mismatches 17; Indels 34; Gaps 7;  
QY 33 TAPCSRGSSWSADLDKCMDCA-SCRRPHSDFCGLCAAAPPAPFRLWPILG-----GAL 86  
Db 235 TAPCS-----CQDCSIVCGPKPQ-----PPPPAP-----WTILGLDAMYVIM 272  
QY 87 SLTFVLGLL-----SGFLVWRCRRER 108  
Db 273 WITYMAFLVFFGFAFFAVW--CYRKR 296

RESULT 9  
FBN1\_MOUSE  
ID FBN1\_MOUSE STANDARD; PRT; 2871 AA.  
AC Q61554; Q60826;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)



DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrillin 1 precursor.  
GN FBN1 OR FBN-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95130561; PubMed=7829516;  
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Pangilinan T.,  
RA Pereira L., Ramirez F., Bonadio J.;  
RT "Primary structure and developmental expression of Fbn-1, the mouse  
RT fibrillin gene.";  
RL J. Biol. Chem. 270:1798-1806(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CD-1; TISSUE=Kidney;  
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
CC -!- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER  
CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE  
CC MICROFIBRILS (BY SIMILARITY).  
CC -!- SIMILARITY: Contains 47 EGF-like domains.  
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.  
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DR EMBL; L29454; AAA56840.1; -.  
DR EMBL; U22493; AAA64217.1; -.  
DR PIR; A55624; A55624.  
DR HSSP; P35555; 1APJ.  
DR MGD; MGI:95489; Fbn1.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002212; Fibril-assoc.  
DR Pfam; PF00008; EGF; 46.  
DR Pfam; PF00683; TB; 9.  
DR SMART; SM00179; EGF\_CA; 42.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 43.  
DR PROSITE; PS00022; EGF\_1; 2.  
DR PROSITE; PS01186; EGF\_2; 38.  
DR PROSITE; PS01187; EGF\_CA; 43.  
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
KW Repeat; Signal; Multigene family.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 2871 FIBRILLIN 1.  
FT DOMAIN 81 112 EGF-LIKE 1.  
FT DOMAIN 115 146 EGF-LIKE 2.  
FT DOMAIN 147 178 EGF-LIKE 3.  
FT DOMAIN 246 287 EGF-LIKE 4.  
FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.  
FT DOMAIN 330 401 TGFBP 1.  
FT DOMAIN 402 446 PRO-RICH.  
FT DOMAIN 449 489 EGF-LIKE 6.  
FT DOMAIN 490 529 EGF-LIKE 7, CALCIUM-BINDING.  
FT DOMAIN 530 571 EGF-LIKE 8, CALCIUM-BINDING.  
FT DOMAIN 572 612 EGF-LIKE 9, CALCIUM-BINDING.  
FT DOMAIN 613 653 EGF-LIKE 10, CALCIUM-BINDING.  
FT DOMAIN 656 721 TGFBP 2.  
FT DOMAIN 723 764 EGF-LIKE 11, CALCIUM-BINDING.  
FT DOMAIN 765 806 EGF-LIKE 12, CALCIUM-BINDING.  
FT DOMAIN 807 846 EGF-LIKE 13, CALCIUM-BINDING.  
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: May facilitate PTTG1 nuclear translocation.  
CC -!- SUBUNIT: Interacts with PTTG1.  
CC -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the  
CC cytoplasm and in the nucleus. According to Ref.1, it is a type I  
CC membrane protein.  
CC -!- TISSUE SPECIFICITY: Ubiquitous.  
CC  
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CC EMBL; Z50022; CAA90325.1; -;  
CC EMBL; AF149785; AAF73770.1; -;  
CC EMBL; AL163300; CAB90552.1; -;  
CC EMBL; BC000415; AAH00415.1; -;  
CC EMBL; BC012858; AAH12858.1; -;  
CC EMBL; BC019295; AAH19295.1; -;  
CC EMBL; BC020983; AAH20983.1; -;  
CC Genew; HGNC:13524; PTTG1IP.  
CC MIM; 603784; -;  
CC GO; GO:0005737; C:cytoplasm; IDA.  
CC GO; GO:0005634; C:nucleus; IDA.  
CC GO; GO:0006606; P:protein-nucleus import; IDA.  
CC InterPro; IPR003659; Plexin-like.  
CC SMART; SM00423; PSI; 1.  
CC Transmembrane; Nuclear protein.  
CC TRANSMEM 97 117 POTENTIAL.  
CC DOMAIN 116 121 POLY-CYS.  
CC CONFLICT 9 19 PTPYRLRLIGG -> ARRTGGCASV (IN REF. 2).  
CC CONFLICT 108 114 TLLLGIA -> NPPPGHC (IN REF. 2).  
CC SEQUENCE 180 AA; 20323 MW; FIE66014D49EC1DE CRC64;  
Query Match 11.3%; Score 69; DB 1; Length 180;  
Best Local Similarity 25.8%; Pred. No. 7;  
Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;  
QY 10 LRLVLGLWLLRLSVAGEQAPGAPCSRGSWSADLDKCMDCASCRARPHSDFCLG--- 66  
Db 15 LRLGGAALLLLLPVAAAEPPGAA-CSQNTNKC--EECLKNVSLWCNTNKACLDYPV 71  
QY 67 CAAPAP-----FRLW-----PILGALSITFVLGSLSGFLVWRRCRRER 108  
Db 72 TSVLPASLCKLSSARWGVGVNFEALITMSVVG-----TLLLGI--AICCCCCRRKR 125  
QY 109 SSPP 112  
Db 126 SRKP 129  
RESULT 14  
Y127\_HUMAN  
ID Y127\_HUMAN STANDARD; PRT; 314 AA.  
AC Q14140;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein KIAA0127.  
GN KIAA0127.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=96127530; PubMed=8590280;  
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;  
RT "Prediction of the coding sequences of unidentified human genes. IV.  
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by  
RT analysis of cDNA clones from human cell line KG-1.";  
RL DNA Res. 2:167-174(1995).  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; D50917; BAA09476.1; -;  
CC Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 314 AA; 33896 MW; E43107FC565AAC31 CRC64;  
Query Match 11.3%; Score 69; DB 1; Length 314;  
Best Local Similarity 34.0%; Pred. No. 12;  
Matches 18; Conservative 6; Mismatches 27; Indels 2; Gaps 1;  
QY 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGCAAPAPFRLLWPIL 82  
Db 112 SPSSHPCDLGS--TTPLEACLTASLLEDDDTFTCSQAMQPTAPTKLSPPAL 162  
RESULT 15  
TNR6\_RAT  
ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL  
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen  
DE (CD95)).  
GN TNFRSF6 OR PT1 OR FAS.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=94128114; PubMed=7507668;  
RA Kimura K., Yamamoto M., Wakatsuki T.;  
RT "A variant mRNA species encoding a truncated form of Fas antigen in  
RT the rat liver.";  
RL Biochem. Biophys. Res. Commun. 198:666-674(1994).  
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD  
CC recruits caspase-8 to the activated receptor. The resulting death-  
CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
CC activation which initiates the subsequent cascade of caspases  
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
CC mediated apoptosis may have a role in the induction of peripheral  
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
CC both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC  
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:35:58 ; Search time 34 Seconds  
(without alignments)  
865.235 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRLLRLVGLWLA.....LSGFLVMRRRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	14.3	333	4	Q9BZG3
2	87	14.3	426	4	Q9BZG2
3	83.5	13.7	610	10	Q943G8
4	79	13.0	341	6	Q9N0B3
5	78.5	12.9	332	10	Q42839
6	78.5	12.9	387	11	Q8VD70
7	77.5	12.7	219	11	Q8BM15
8	76.5	12.6	245	16	Q8Z5R3
9	75.5	12.4	222	12	Q9QEE6
10	75.5	12.4	449	16	O53668
11	75.5	12.4	635	5	O18288
12	75	12.3	370	4	Q96KN9
13	75	12.3	411	16	Q8CXG1
14	74.5	12.3	519	16	Q9A9X4
15	74	12.2	548	11	Q8K406
16	74	12.2	768	5	P90890

17	73.5	12.1	730	4	Q9P2P7	Q9p2p7 homo sapien
18	73	12.0	227	10	O04393	O04393 hordeum vul
19	73	12.0	243	16	Q8PQD6	Q8pqd6 xanthomonas
20	73	12.0	370	4	Q8N2R7	Q8n2r7 homo sapien
21	73	12.0	768	13	Q98TH8	Q98th8 cyprinus ca
22	72.5	11.9	206	4	Q96QA0	Q96qa0 homo sapien
23	72.5	11.9	242	16	Q8NNC0	Q8nnc0 corynebacte
24	72.5	11.9	329	4	Q9NQD2	Q9nqd2 homo sapien
25	72.5	11.9	346	16	Q9RSC0	Q9rsc0 deinococcus
26	72.5	11.9	365	4	Q9Y288	Q9y288 homo sapien
27	72.5	11.9	370	4	Q9BZW8	Q9bzw8 homo sapien
28	72	11.8	368	13	Q9IAR7	Q9iar7 gallus gall
29	72	11.8	721	5	Q8I8V6	Q8i8v6 giardia lam
30	71.5	11.8	210	4	O95054	O95054 homo sapien
31	71.5	11.8	379	10	Q8W393	Q8w393 oryza sativ
32	71.5	11.8	2873	12	O93072	O93072 hepatitis g
33	71	11.7	116	12	O90631	O90631 baboon herp
34	71	11.7	175	16	Q9S255	Q9s255 streptomyce
35	71	11.7	473	16	Q98J10	Q98j10 rhizobium l
36	71	11.7	557	11	Q9QZF2	Q9qzf2 mus musculu
37	71	11.7	646	10	Q8RZP4	Q8rzp4 oryza sativ
38	70.5	11.6	204	16	Q8P3W7	Q8p3w7 xanthomonas
39	70.5	11.6	412	16	Q9FCA1	Q9fca1 streptomyce
40	70.5	11.6	467	16	Q92X93	Q92x93 rhizobium m
41	70	11.5	127	4	Q96LP0	Q96lp0 homo sapien
42	70	11.5	206	15	Q75637	Q75637 human immun
43	70	11.5	243	16	Q8PDE9	Q8pde9 xanthomonas
44	70	11.5	293	6	Q9TTI0	Q9ttt0 sus scrofa
45	70	11.5	301	4	Q9UJA2	Q9uja2 homo sapien

ALIGNMENTS

RESULT 1  
Q9BZG3 ID Q9BZG3 PRELIMINARY; PRT; 333 AA.  
AC Q9BZG3;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Acid phosphatase variant 3.  
GN ACPT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21309073; PubMed=11414767;  
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;  
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis."  
RL Genomics 74:385-395(2001).  
DR EMBL; AF321918; AAK09396.1; --  
DR HSSP; P15309; 2HPA.  
DR InterPro; IPR000560; HisAc\_phsphtse.  
DR Pfam; PF00328; acid\_phosphat; 1.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 14.3%; Score 87; DB 4; Length 333;  
Best Local Similarity 35.3%; Pred. No. 0.45;  
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY	31	PG-TAPCSRGSSWSADLDKCMDCASCARPHSDFCLGC--AAAPPAPFRLLPILGGALS	87
Dd	258	PGCPAPCPLGRFYQL-----TAPAPPAHGVSCHGPEAIPAP---VVPLLAGAVA	307
QY	88	LTFVLGLLSGFLVWR-RCRRRSSP	111
Dd	308	VLVALSIGLGLAWRPGCLRALGGP	332







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RESULT 8
Q8Z5R3
ID Q8Z5R3 PRELIMINARY; PRT; 245 AA.
AC Q8Z5R3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Flagellar biosynthetic protein Flp.
GN STY2187.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
DR EMBL; AL627272; CAD05727.1; -
DR InterPro; IPR005837; Flp.
DR InterPro; IPR005838; TypeIII_P.
DR Pfam; PF00813; Flp; 1.
DR PRINTS; PR01302; TYPE3IMPPROT.
DR ProDom; PD002586; TypeIII_P; 1.
DR TIGRFAMS; TIGR01103; flp; 1.
DR PROSITE; PS01060; FLIP_1; 1.
DR PROSITE; PS01061; FLIP_2; 1.
DR Complete proteome.
KW SEQUENCE 245 AA; 26755 MW; C9B9931F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 16; Length 245;
Best Local Similarity 30.8%; Pred. No. 4.1;
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRLRLLLVLGLWLLRLSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRA-- 59
:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRLLFLSLAGLW--LFSPAAQAQLPGLISQPLAGGQSWLSVQTLVFTSLTFLPAIL 58
:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 --HSDF-----CLGCAAPAPFRLLLWPILGGALSFTVL 92
:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 LMWTSFTRIIIVFGLLRNALGTPSAPPNQV-----LLGLALFLTFFI 100
:|||||:|||||:|||||:|||||:|||||:|||||:
```

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RESULT 9
Q9QEE6
ID Q9QEE6 PRELIMINARY; PRT; 222 AA.
AC Q9QEE6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 23kDa protein (Putative 23 kDa nucleic acid binding protein).
OS Indian citrus ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
OX NCBI_TaxID=104664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=20496665; PubMed=11043949;
RA Rustici G., Accotto G.P., Norris E., Masenga V., Luisoni E.,
RA Milne R.G.;
RT "Indian citrus ringspot virus: a proposed new species with some
RT affinities to potex-, carla-, fovea- and allexiviruses.";
RL Arch. Virol. 145:1895-1908 (2000).

Query Match 12.4%; Score 75.5; DB 16; Length 449;
Best Local Similarity 23.0%; Pred. No. 9.2;
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Rustici G., Milne R.G., Accotto G.P.;
RT "Nucleotide sequence, genome organization and phylogenetical analysis
RT of Indian citrus ringspot virus.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184962; AAF01314.1; -
DR EMBL; AF406744; AAK97527.1; -
SQ SEQUENCE 222 AA; 25455 MW; 636A47058DD8D01D CRC64;

Query Match 12.4%; Score 75.5; DB 12; Length 222;
Best Local Similarity 35.4%; Pred. No. 4.7;
Matches 35; Conservative 7; Mismatches 38; Indels 19; Gaps 7;

QY 3 RGSIRRLRLLLVLGLWLLRLSVAGEQAP-GTAPCSRGSWSADLDKCMDCASCRA--RP 59
:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 RGSQIRSVRLLP---WRPFRFPV---CPSGTSPYSRGTHSQPSYVRCQNCERARQWFERA 74
:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 H-SDFCL-----GCAAPAPFRLLL---WPILGGALS 88
:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 HDGPRCLHQRPDYSRLQAPDPDFQHLNSFEPILLALSLV 113
:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 10
O53668
ID O53668 PRELIMINARY; PRT; 449 AA.
AC O53668;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative membrane protein.
GN RV0246 OR MT0260 OR MTV034.12.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
```

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RESULT 9
Q9QEE6
ID Q9QEE6 PRELIMINARY; PRT; 222 AA.
AC Q9QEE6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 23kDa protein (Putative 23 kDa nucleic acid binding protein).
OS Indian citrus ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
OX NCBI_TaxID=104664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=20496665; PubMed=11043949;
RA Rustici G., Accotto G.P., Norris E., Masenga V., Luisoni E.,
RA Milne R.G.;
RT "Indian citrus ringspot virus: a proposed new species with some
RT affinities to potex-, carla-, fovea- and allexiviruses.";
RL Arch. Virol. 145:1895-1908 (2000).
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QY 1 MARGSLRLRLRLVLGLWLLLRVAGEQA--PGTAPCSRGS--WSADLDKCMDCASC 56
Db 155 MPSTARARILLTEVGVAALTAVVAATLSFVPDQHPLSRNHLLWTAAVAMASAAICR 214
QY 57 ARPHSDFCLGCAAAAPPAPFRLW-----PILGG----- 84
Db 215 ALPHR--IVPRVHAAPGLHKLKLVVGWTAIRNGWYRRYLLVQLVFGSVLGSFHSIRVA 272
QY 85 -----ALSLTFVLGLLSGFLVWRRCR 105
Db 273 AVPGDQDPDEVAVVAVVLCVGLLGGIALWNRVR 304

RESULT 11
O18288
ID O18288 PRELIMINARY; PRT; 635 AA.
AC O18288;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ZK1010.9 protein.
GN ZK1010.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A., McMurray A.; to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81503; CAB04115.1; -.
DR EMBL; Z82083; CAB04115.1; JOINED.
DR EMBL; Z82083; CAB04975.1; -.
DR EMBL; Z81503; CAB04975.1; JOINED.
DR WormPep; ZK1010.9; CE23490.
DR InterPro; IPR000175; Na/ntran_sympoirt.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_sympoirt; 1.
DR PROSITE; PS05267; NA_NEUROTRAN_SYMP_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 635 AA; 71267 MW; 2841834039D8F14A CRC64;

Query Match 12.4%; Score 75.5; DB 5; Length 635;
Best Local Similarity 36.6%; Pred. No. 13;
Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;

QY 31 PGTAPCSRGSWSADLDKCMDCASCRRP--HSDFLG--CAAAAPPAPFRLWLPILGGAL 86
Db 92 PTTAYKNGGLSF---LIAYVVGILFAVPAIHMEFALGQYAAKSPPAAFRRMPILGVG 148

QY 87 SLTFVLGLLSG 97
Db 149 WMTCLVGAIG 159

RESULT 12
Q96KN9
ID Q96KN9 PRELIMINARY; PRT; 370 AA.
AC Q96KN9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Connexin40.1 (Gap junction protein).
GN CX40.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eiberger J., Soehl G., Willecke K.;
```

```
RT "Structural and functional diversity of connexin genes in the mouse
RT and human genome.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
CC (BY SIMILARITY).
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
DR EMBL; AJ414564; CAC93846.1; -.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 12.3%; Score 75; DB 4; Length 370;
Best Local Similarity 27.9%; Pred. No. 8.6;
Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;

QY 9 LLRLVLGLWLLLRVAGEQAQGTAPCSRGSWSADLDKCMDCASCRRPHSDFCLGCA 68
Db 148 LLRTLLAAFGALHYFLFGFLAPKKFPCT-----RPFCTGVVDCY 187

QY 69 AAPAPFRLWLPILGGALSLTFVLGLLSGFLVWRRCRERRSSPP 112
Db 188 VSRPTEKSLMLFLWAVSALSFLGLADLVCSLRRRMRRRPGPP 231

RESULT 13
Q8CXG1
ID Q8CXG1 PRELIMINARY; PRT; 411 AA.
AC Q8CXG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Multidrug resistance protein (Efflux transporter).
GN OB1706.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004598; BAC13662.1; -.
KW Complete proteome.
SQ SEQUENCE 411 AA; 45188 MW; 589B48F6EC39275A CRC64;

Query Match 12.3%; Score 75; DB 16; Length 411;
Best Local Similarity 27.6%; Pred. No. 9.5;
Matches 32; Conservative 13; Mismatches 33; Indels 38; Gaps 5;

QY 17 LWLALLRSVAGEQAQGTAPCS-----RGSSWSADLDKCMDCASCRRPHSDFCLGCA 68
Db 102 IWLIGRIIQIGAGCTFPIAMALIGDLFKGSESK-----MLGIY 142

QY 69 AAPAPFRLWLPILGGALSL-----TF-VLGLLSGFLV--WRRCRERRSSPP 113
Db 143 EASNELGKVLSPIIIGAALITWYFVFTFPVLSLCAILVFFFIKERRNRQTPEP 198

RESULT 14
```

Q9A9X4 Q9A9X4 PRELIMINARY; PRT; 519 AA.  
AC Q9A9X4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein CC0837.  
GN CC0837.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_TaxID=155892;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA DeBoy R.T., Dodson R.J., Durkin A.S., Winn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
DR EMBL; AE005760; AAK22822.1; -.  
DR TIGR; CC0837; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;  
  
Query Match 12.3%; Score 74.5; DB 16; Length 519;  
Best Local Similarity 24.3%; Pred. No. 13;  
Matches 33; Conservative 21; Mismatches 51; Indels 31; Gaps 4;  
  
QY 9 LLRLVLGLWLLRS-VAGEQAPGTAPCSRGS-----SWSADLDKCMD 51  
Db 250 LLILMAIGLGLFLFAAQVLGRFADAAATQGAETRKAAGKGPVGAFAAGAFQATLRKELR 309  
  
QY 52 CASCRARPHSDFCLGCAAPAPFRL-----WPILGGALSLTFVLGSLGFLVWR 103  
Db 310 LVSRDAALLSQVLLRLVLMVPIAFVMVGAESLPWALAGPAAAVTFLAGOVAGSLIWIT 369  
  
QY 104 CRRERS-----SPPP 113  
Db 370 VSAEDTPDLLAISPTP 385

RESULT 15  
Q8K406 Q8K406 PRELIMINARY; PRT; 548 AA.  
AC Q8K406;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Leubrin/leucine-rich glioma inactivated 1-like protein (Weakly similar  
DE to leucine-rich glioma-INACTIVATED 1 protein).  
GN LGI3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Yun H.-Y., Lee S.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AF515590; AAM55219.1; -.  
DR EMBL; AK049831; BAC33943.1; -.  
DR MGD; MGI:2182619; Lgi3.  
DR InterPro; IPR005492; EPTP.  
DR InterPro; IPR000566; Lipocln\_cytFABP.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR003591; LRR\_typ.  
DR Pfam; PF03736; EPTP; 2.  
DR Pfam; PF00560; LRR; 1.  
DR Pfam; PF01463; LRRCT; 1.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00369; LRR\_TYP; 3.  
DR PROSITE; PS00213; LIPOCALIN; 1.  
DR PROSITE; PS50506; LRR\_TYPICAL; 1.  
SQ SEQUENCE 548 AA; 61817 MW; 2DB303936354B958 CRC64;  
  
Query Match 12.2%; Score 74; DB 11; Length 548;  
Best Local Similarity 40.4%; Pred. No. 16;  
Matches 21; Conservative 5; Mismatches 24; Indels 2; Gaps 1;  
  
QY 3 RGSRLRLRLLLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCAS 54  
Db 8 RGPGRLLVLSTLGFCLML--QVSAKRPPKTPPCPPSCSCTRDTAFCVDSKS 57  
  
Search completed: February 11, 2004, 10:39:21  
Job time : 37 secs

GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: February 11, 2004, 10:37:18 ; Search time 21 Seconds  
(without alignments)  
229.688 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLLLVLGLWLA.....LSGFLVWRCRRRSSPPPX 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	274.5	45.1	155	4	US-09-489-847-284
4	274.5	45.1	156	4	US-09-489-847-228
5	96.5	15.9	248	4	US-09-252-991A-29249
6	88.5	14.6	400	4	US-09-252-991A-26145
7	87.5	14.4	631	4	US-09-252-991A-20063
8	83.5	13.7	152	4	US-09-252-991A-31619
9	80.5	13.2	249	4	US-09-252-991A-29850
10	76.5	12.6	250	4	US-09-322-409-31
11	76.5	12.6	250	4	US-09-451-527-31
12	76.5	12.6	276	4	US-09-322-409-26
13	76.5	12.6	276	4	US-09-451-527-26
14	75	12.3	334	4	US-09-252-991A-18795
15	74.5	12.3	305	4	US-09-252-991A-21147
16	73.5	12.1	187	4	US-09-199-637A-287
17	73.5	12.1	187	4	US-09-252-991A-21454
18	72	11.8	1278	4	US-09-462-136-2
19	72	11.8	3724	2	US-08-804-227C-10
20	72	11.8	3724	2	US-08-804-198-4
21	71.5	11.8	478	4	US-09-252-991A-22078
22	70.5	11.6	402	4	US-09-252-991A-18195
23	70	11.5	720	4	US-09-996-243-231
24	69.5	11.4	176	4	US-09-252-991A-25290
25	69	11.3	152	4	US-09-252-991A-24730
26	69	11.3	153	4	US-09-252-991A-20688
27	69	11.3	215	3	US-09-220-528-104

28	69	11.3	511	4	US-09-252-991A-28223	Sequence 28223, A
29	68.5	11.3	205	2	US-08-775-009-37	Sequence 37, Appl
30	68.5	11.3	429	1	US-07-964-589-2	Sequence 2, Appli
31	68.5	11.3	429	5	PCT-US93-02024-2	Sequence 2, Appli
32	68	11.2	139	4	US-09-252-991A-17414	Sequence 17414, A
33	68	11.2	144	4	US-09-252-991A-17313	Sequence 17313, A
34	68	11.2	204	4	US-09-252-991A-29996	Sequence 29996, A
35	68	11.2	282	4	US-09-252-991A-29124	Sequence 29124, A
36	68	11.2	366	4	US-09-252-991A-31958	Sequence 31958, A
37	68	11.2	775	4	US-09-252-991A-22300	Sequence 22300, A
38	67.5	11.1	174	3	US-09-383-586-12	Sequence 12, Appl
39	67.5	11.1	268	4	US-09-322-409-23	Sequence 23, Appl
40	67.5	11.1	268	4	US-09-451-527-23	Sequence 23, Appl
41	67.5	11.1	294	4	US-09-322-409-7	Sequence 7, Appli
42	67.5	11.1	294	4	US-09-451-527-7	Sequence 7, Appli
43	67.5	11.1	359	3	US-09-413-814-90	Sequence 90, Appl
44	67.5	11.1	361	3	US-09-413-814-77	Sequence 77, Appl
45	67	11.0	112	4	US-09-252-991A-21707	Sequence 21707, A

ALIGNMENTS

RESULT 1  
US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 99.8%; Score 607; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4.5e-59;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARGSLRRLRLLLVLGLWALLRSVAGEAPGTAPCSRGSSWSADLDKCMDASCRRPH 60  
Db 1 MARGSLRRLRLLLVLGLWALLRSVAGEAPGTAPCSRGSSWSADLDKCMDASCRRPH 60



QY 61 SDFCLGCAAAAPPAPFRLLWPILGALSLTFVLGLLSGFLVWRRERRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLWPILGALSLTFVLGLLSGFLVWRRERRSSPPP 113

RESULT 2  
US-09-489-847-139  
; Sequence 139, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-139

Query Match 45.1%; Score 274.5; DB 4; Length 112;  
Best Local Similarity 96.4%; Pred. No. 9e-23;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 3  
US-09-489-847-284  
; Sequence 284, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 284  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-284

Query Match 45.1%; Score 274.5; DB 4; Length 155;  
Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 4  
US-09-489-847-228  
; Sequence 228, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 228  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (156)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-489-847-228

Query Match 45.1%; Score 274.5; DB 4; Length 156;  
Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
Db 1 MARGSLRRLRLLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 5  
US-09-252-991A-29249  
; Sequence 29249, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29249  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

Query Match	14.4%;	Score 87.5;	DB 4;	Length 631;
Best Local Similarity	32.6%;	Pred. No. 0.17;		
Matches	30;	Conservative	6;	Mismatches 43; Indels 13; Gaps 4;
QY	23	RSVAGEQAPGTAPCRGS-SWS-ADLDKCM--DCASCRARPHSDFCGLGCAAPAPPRILL	78	

RESULT 9  
US-09-252-991A-29850  
; Sequence 29850, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29850  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29850

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Query Match      13.2%; Score 80.5; DB 4; Length 249;
Best Local Similarity 30.5%; Pred. No. 0.35;
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QY 58 RP-----HSDFCIGCA-AAPPAPRLLW-----PILGGALSLTFVLGSLGFLV 100  
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QY 101 WRCRRRSSP 111  
Db 206 ----RTRRSAP 212

RESULT 10  
US-09-322-409-31  
; Sequence 31, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-322-409-31

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Best Local Similarity 27.5%; Pred. No. 0.95;  
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Db 49 RLVLQRMVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 108  
QY 45 DLD-KCMDCASCRRPHSDFCIGCAA--APPAPERLLWPILGGALSLTFVLGSLGFLV 101  
Db 109 CLELQCQPDSSSTLVPPRSPGAEATAPAPQAP-RLLLLL---LPVALLMSTAWCLHW 164  
QY 102 RRCRRRSSP 112  
Db 165 RRRRRRSSPYP 175

RESULT 11  
US-09-451-527-31  
; Sequence 31, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 250  
; TYPE: PRT

; ORGANISM: Canis familiaris  
US-09-451-527-31  
Query Match 12.6%; Score 76.5; DB 4; Length 250;  
Best Local Similarity 27.5%; Pred. No. 0.95;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;  
QY 11 RLLVLGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
Db 49 RLVLQRMVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 108  
QY 45 DLD-KCMDCASCRRPHSDFCIGCAA--APPAPERLLWPILGGALSLTFVLGSLGFLV 101  
Db 109 CLELQCQPDSSSTLVPPRSPGAEATAPAPQAP-RLLLLL---LPVALLMSTAWCLHW 164  
QY 102 RRCRRRSSP 112  
Db 165 RRRRRRSSPYP 175

RESULT 12  
US-09-322-409-26  
; Sequence 26, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-322-409-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;  
Best Local Similarity 27.5%; Pred. No. 1.1;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;  
QY 11 RLLVLGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
Db 75 RLVLQRMVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 134  
QY 45 DLD-KCMDCASCRRPHSDFCIGCAA--APPAPERLLWPILGGALSLTFVLGSLGFLV 101  
Db 135 CLELQCQPDSSSTLVPPRSPGAEATAPAPQAP-RLLLLL---LPVALLMSTAWCLHW 190  
QY 102 RRCRRRSSP 112  
Db 191 RRRRRRSSPYP 201

RESULT 13  
US-09-451-527-26  
; Sequence 26, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2





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OM protein - protein search, using sw model

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Title: US-10-062-599-59  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA: \*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW PUB.pep: \*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW PUB.pep: \*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	99.8	114	12	Sequence 59, Appl
2	607	99.8	114	15	Sequence 59, Appl
3	571	93.9	129	9	Sequence 4, Appl
4	571	93.9	129	10	Sequence 4, Appl
5	571	93.9	129	12	Sequence 178, App
6	571	93.9	129	12	Sequence 178, App
7	571	93.9	129	12	Sequence 37, Appl
8	571	93.9	129	12	Sequence 444, App
9	571	93.9	129	12	Sequence 1305, App
10	450	74.0	129	9	Sequence 5, Appl
11	450	74.0	129	10	Sequence 5, Appl
12	433	71.2	309	9	Sequence 7, Appl
13	433	71.2	309	10	Sequence 7, Appl
14	379.5	62.4	300	10	Sequence 9, Appl
15	97.5	16.0	171	15	Sequence 4, Appl

16	97.5	16.0	171	15	US-10-251-947-7	Sequence 7, Appl
17	97.5	16.0	185	15	US-10-251-947-2	Sequence 2, Appl
18	97	16.0	170	15	US-10-251-947-6	Sequence 6, Appl
19	96.5	15.9	186	15	US-10-251-947-14	Sequence 14, Appl
20	88.5	14.6	1307	15	US-10-303-685-17	Sequence 17, Appl
21	88.5	14.6	1388	12	US-10-093-463-138	Sequence 138, App
22	88.5	14.6	1388	12	US-10-093-463-140	Sequence 140, App
23	87	14.3	184	15	US-10-008-063-2	Sequence 2, Appl
24	87	14.3	184	15	US-10-152-363A-60	Sequence 60, Appl
25	79.5	13.1	377	15	US-10-156-761-8962	Sequence 8962, Ap
26	76.5	12.6	250	12	US-10-262-439-31	Sequence 31, Appl
27	76.5	12.6	250	15	US-10-218-654-31	Sequence 31, Appl
28	76.5	12.6	276	12	US-10-262-439-26	Sequence 26, Appl
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33	75.5	12.4	635	12	US-10-369-493-5911	Sequence 5911, Ap
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35	75	12.3	356	12	US-10-085-198-64	Sequence 64, Appl
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39	73.5	12.1	409	15	US-10-156-761-11890	Sequence 11890, A
40	72.5	11.9	242	10	US-09-738-626-6004	Sequence 6004, Ap
41	72.5	11.9	365	11	US-09-860-836B-5	Sequence 5, Appl
42	72.5	11.9	365	12	US-10-436-523-59	Sequence 59, Appl
43	72.5	11.9	391	12	US-10-264-049-2579	Sequence 2579, Ap
44	72	11.8	257	12	US-10-104-047-3192	Sequence 3192, Ap
45	72	11.8	1278	15	US-10-208-731-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-062-599-59  
; Sequence 59, Application US/10062599  
; Publication No. US20030195346A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: P2006P1  
; CURRENT APPLICATION NUMBER: US/10/062,599  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens

```

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match      99.8%; Score 607; DB 12; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||
Db 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||

QY 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
    |||||
Db 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
    |||||

RESULT 2
US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006PI
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match      99.8%; Score 607; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||
Db 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||

QY 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
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*Handwritten signature*

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Db 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      93.9%; Score 571; DB 9; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||
Db 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||

QY 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
    |||||
Db 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
    |||||

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      93.9%; Score 571; DB 10; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||
Db 1 MARGSLRRLRLRLVGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRARPH 60
    |||||

QY 61 SDFCLGCAAAPAPFRLWPILGALSITFVLGSLSGFLVWRRRERSSSPPP 113
    |||||
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Db 61 SDFCLGCAAPAPFRLLWPILGGALSLTFVLGSLSGFLVWRRRCRRREKFTTP 113

RESULT 5

US-10-024-298A-178  
; Sequence 178, Application US/10024298A  
; Publication No. US20030143540A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA  
; APPLICANT: AKIO MATSUDA  
; APPLICANT: Goichi HONDA  
; APPLICANT: Shuji MURAMATSU  
; APPLICANT: Yukiko NAGANO  
; TITLE OF INVENTION: NF-K B Activating Gene  
; FILE REFERENCE: 1254-0191P  
; CURRENT APPLICATION NUMBER: US/10/024,298A  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/278,641  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP0088912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-298A-178

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
QY 61 SDFCLGCAAPAPFRLLWPILGGALSLTFVLGSLSGFLVWRRRCRRRSPP 113  
Db 61 SDFCLGCAAPAPFRLLWPILGGALSLTFVLGSLSGFLVWRRRCRRREKFTTP 113

RESULT 6

US-10-042-211A-178  
; Sequence 178, Application US/10042211A  
; Publication No. US20030170719A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFkB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24

; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-211A-178

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
QY 61 SDFCLGCAAPAPFRLLWPILGGALSLTFVLGSLSGFLVWRRRCRRRSPP 113  
Db 61 SDFCLGCAAPAPFRLLWPILGGALSLTFVLGSLSGFLVWRRRCRRREKFTTP 113

RESULT 7

US-10-331-496A-37  
; Sequence 37, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WU, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; FILE REFERENCE: P5014R1-PCT  
; CURRENT APPLICATION NUMBER: US/10/331,496A  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/345,444  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US 60/351,885  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/360,066  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US 60/362,004  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/366,869  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,284  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/368,679  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 37  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-331-496A-37

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60  
Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRREKFTTP 113

RESULT 8

US-10-295-027-444  
; Sequence 444, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynné, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 444  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-444

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRREKFTTP 113

RESULT 9

US-10-295-027-1305  
; Sequence 1305, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynné, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1305  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-1305

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRRLRLVLGLWLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
QY 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRSSPPP 113  
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSALTFLVGLLGSFLVWRRRRREKFTTP 113

RESULT 10

US-09-742-454A-5  
; Sequence 5, Application US/09742454A  
; Patent No. US20020041876A1  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5



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; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match      74.0%; Score 450; DB 9; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.2e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
Db 1 MAPGWPRSLPQILVGLFGLVLMRAAAGEQAPGTSPCSSGSSWSADLDKCMDCASCRARPH 60
QY 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 113
Db 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 113

RESULT 11
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match      74.0%; Score 450; DB 10; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.2e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
Db 1 MAPGWPRSLPQILVGLFGLVLMRAAAGEQAPGTSPCSSGSSWSADLDKCMDCASCRARPH 60
QY 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 113
Db 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 113

RESULT 12
US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. US2002041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match      71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.5e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
Db 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
QY 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 112
Db 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 112

RESULT 13
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match      71.2%; Score 433; DB 10; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.5e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
Db 1 MARGSLRRLRLLLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
QY 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 112
Db 61 SDFCLGCAAAPPAHFRLLWPILGGALSITFVLGSLGFLVWRRRERSPPPP 112

RESULT 14
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; APPLICANT: Wiley, Steven R.
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